Schreiber, David

From:

Ramirez, Delia

Sent:

Friday, April 15, 2005 6:51 PM

To:

Schreiber, David

Subject:

case 10/652334

Hi,

I would like to request the following search (commercial and interference): SEQ ID NO:1-9 in the protein databases.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

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FOR OFFICIAL USE ONLY

ACCESS DB #	
	PRINT CLEARLY

Scientific and Technical Information Center

SEARCH REQUEST FORM

Doquecter's Full Name		Examiner #:	Date:
Art Unit: Phor	ne Number: 2-	Serial Number	
Requester's Full Name: Art Unit: Phor Location (Bldg/Room#): *******************************	_ (Mailbox #):	Results Format Prefer	ed (circle): PAPEK DISK
**********	*******	******	**************************************
To ensure an efficient and quality searc	ch, please attach a copy o	f the cover sheet, claims, and abstr	act or fill out the following:
			•
Title of Invention:			
Inventors (please provide full name	s):		
Earliest Priority Date:			
Search Topic: Please provide a detailed statement of the elected species or structures, keywords, so Define any terms that may have a special			
For Sequence Searches Only Please appropriate serial number.	include all pertinent infor	mation (parent, child, divisional, or	issued patent numbers) along with the
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STAFF USE ONLY	Type of Searc	h Vendors an	d cost where applicable
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Identifying an agent that increases nonsense suppression, for anti-
therapy, by contacting modulator of translation termination (Mtt1)
Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                                                                                                                                                                                                                                        therapy; HCSB; nonsense mutation; yeast.
                                                              Disclosure; Col 41; Opp; English.
                                                                             binding to Mttl.
                                                                                                                      WPI; 2003-810549/76.
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                                                                                              for antiviral on (Mttl) in
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The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide

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         the RNA helicase MTT1 with a composition or agent under conditions permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1. The composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, permit monitoring of a termination event, promote degradation of aberrant
                                                                                                                                                                                                   Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTTI with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9
                                                                                                                       The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting
                                                                                                                                                                                                                                                             WPI; 2004-449400/42
                                                                                                                                                                                                                                                                                                                              (PELT/)
(CZAP/)
                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1998;
22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis;
Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa;
Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; translation termination; RNA helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP44103 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia
Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast translation termination modulation protein motif
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                                                                                                                                                                                                                                                                                                                ) PELTZ S.
) CZAPLINSKI F
DINMAN J D.
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milarity 100.0%;
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and provide modulators
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99US-00359268
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                                                                                                                                                                NO 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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Pred. No.
                                                                                                                                                                English
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  (inhibitors/stimulators)
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Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transferase activity during initiation, elongation, termination and mRNA degradation of translation. The agents, which may be antagonists or agonists, are useful in screening, diagnostic and therapeutic purposes, for diseases or conditions resulting from or cause premature translation, such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular Dystrophy, Haemophilia B, Haemophilia B, Von Willebrand Disease, osteogenesis Imperfecta, Breast cancer, Ovarian Cancer, Wilms Tumour, Hirschaprung disease, Cystic fibrosis, Kidney Stones, Familial hypercholesterolaemia, Retinitis Pigmentosa, or Neurositoromatosis, Retinoblastoma, ATM or Costmann Disease. The present sequence represents the amino acid sequence of the yeast translation termination modulation
carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                     New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9
                                                                                                The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTIL, for Modulator of Translation Termination) and the conserved proteins known to interact and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY77804 standard; peptide; 10
                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                       WPI; 2000-171458/15
                                                                                                                                                                                                                                                                                                                                                              Peltz S,
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                                                                                                                                                                                                                                                                                                                                                                                                     (UYNE-) UNIV NEW JERSEY
                                                                                                                                                                                                  33; Page 79;
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                                                                                                                                                                                                                                                                                                                                                              Czaplinski K,
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RESULT 4
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CC sequences AAY77804-812 represent motifs I-IX comprised in the genes of interact useful for modulation translation to termination.
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Best Local /
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primer; chromosome mapping; gene mapping; recombinant protein production.
                                                                                                                                                                                                              New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-876918/81.
N-PSDB; ADF58025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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Pred. No.
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The present sequence represents a polypeptide (II) with biological activity, which is encoded by an isolated polynucleotide sequence (I) from the present invention . Also described: (1) a vector comprising

(H)

Sequence 135 AA

Claim 20;

SEQ ID NO 1433; 571pp; English.

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RESULT 5
ABP38224
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (2) an expression vector comprising (I); (3) a host cell genetically engineered to comprise (I) which is operatively associated with a regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4); (9) producing the polypeptide of (4); and (I0) a collection of polymucleotides comprising at least one of the polymucleotide sequences (I). The polymucleotide (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                             ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis; open reading frame; ORP; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 159
                                                                                                                                                                                                                                                                                                                                                                         Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP38224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP38224 standard; protein; 135 AA
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                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                       2002-381255/41.
DB; ABN90769.
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7; Conserv
                                                                                                                                                                                                                              SEQ ID NO 3069; 267pp; English.
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97US-0064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                           Bush D;
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Pred. No. 1.3e
0; Mismatches
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1.3e+02;
2;
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Matches Query Match Best Local

Similarity

78.7**%;** 77.8**%**;

Length 135;

Indels

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Gaps

0

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44 GEPGTKTIT 52

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                                                                                                                                                                                                    CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) can have antibacterial activity and therefore can be used in CC vaccination. The mucleic acids (I) may be used to produce the S. (C epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their CC activity and therefore identify compounds that may be used for the CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polymucleotide sequences from the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the CC exemplification of the present invention. Na. The present invention Specifically claims all the polymucleotide sequences given in the CC sequence listing of the present invention. Na. The present invention cCC sequence listing of the present invention. Naver the sequence CC listing only goes up to SEQ ID NO:4454 so even though sequences are present contained to the contained contained to the sequence are present contained to the contained contained to the contained contained to the contained contained to the present invention. The contained contained to the present invention contained to the contained contained to the present of the present apecification, however the sequence contained contained to the present of the contained to the contained contained contained contained con
                                                                          Matches
                                                                                               Query Match
Best Local 9
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N-PSDB; AAH53475.
                                                                                                                                                              Sequence 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 620; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides from Staphylococcus epidermidis useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG82625 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD
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1 GPPGTKTXT 9
                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPGTKTXT 9
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                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   open reading frame protein sequence SEQ ID NO:2344.
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                                                                                               78.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AA
                                                                        0;
                                                                                               Score 37; DB 4;
Pred. No. 4.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 5; Le Pred. No. 2.3e+02; 0; Mismatches 2;
                                                                          Mismatches
                                                                                               4.4e+02;
                                                                                                                  Length 278;
                                                                          Indels
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                                                                        Gaps
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in AB95124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                          S. epidermidis open reading frame protein sequence SEQ ID NO:2638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis, open reading frame, ORF; bacterial infection, antibacterial, gene therapy.
                                                                             03-SEP-2001 (first entry)
                                                                                                                                          AAG82772 standard; protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                   Sequence 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 3068; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABN90768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP38223 standard; protein; 383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                    Local Similarity 77.8
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                                                                                                                                                                                                                                                     1 GPPGTKTXT 9
                                                                                                                                                                                                                         GEPGIKTIT 91
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                                                                                                                                                                                                                                                                                                   78.7%;
77.8%;
                                                                                                                                                                                                                                                                                                     Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                     6e+02;
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                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                   Length 383;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      0;
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endocarditis.

Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;

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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
 17-MAY-2001.
                                                                 Staphylococcus
                                                                                                                                                   S. epidermidis open reading frame protein sequence SEQ ID NO:2496.
                                                                                                                                                                                     03-SEP-2001
                                                                                                                                                                                                                      AAG82701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-316495/33.
N-PSDB; AAH53622.
                                 WO200134809-A2
                                                                                                                                                                                                                                                    AAG82701 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 692; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kimmerly WJ;
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                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                          GPPGTKTXT 9
                                                                                                                                                                                                                                                                                                                                          GEPGTKTIT 52
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                     (first entry)
                                                                  epidermidis
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 4;
Pred. No. 6.3e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 10
ADG30695
ID ADG30
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Best Local (
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                   ADG30695 standard; protein; 577 AA.
                                                                                                                                                                                                                                                                    Sequence 470 AA;
                                                                                                                                                                                                                                                                                                                         represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 657; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000; 2000WO-US030782
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                                                                                                                                                                                     Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                            SEQ ID NO:4455 to 4464
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                                                                                                                  44
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                                                                                                                                                       1 GPPGTKTXT 9
                                                                                                                  GEPGIKTIT 52
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROUP LTD
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                                                                                                                                                                                                             78.7%;
77.8%;
                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                             Score 37; DB 4; Pred. No. 7.3e+02;
                                                                                                                                                                                                                               Length 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding polypeptides
                                                                                                                                                                                             Indels
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26-FEB-2004
                  22-APR-2002; 2002US-0374620P
                                    22-APR-2003; 2003WO-BR000060
                                                        30-OCT-2003
                                                                           WO2003089647-A1
                                                                                            Xanthomonas axonopodis pv. citri
                                                                                                                        Xanthomonas microorganism; plant; pathology; bacterial pest; Xac; Xcc;
                                                                                                                                            Xanthomonas
                                                                                                                                         axonopodis pv citri plant pathology-related XAC2118 protein.
                                                                                                                                                               (first entry)
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(AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with pathogenicity caused by the Xanthomonas microorganism, or its variant, that causes reduced or enhanced pathogenicity. The nucleic acid of the invention may be useful in detecting the presence of Xanthomonas bacteria in a sample, as well as in plant pathology, for example, for identifying nucleic acid molecules and proteins involved in pathology caused by bacterial pests. The current sequence is that of the Xanthomonas axonopodis pv. citri (Xac) plant pathology-related XAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Da Silva ACR, F
De Oliveira JCF,
         AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis and (II) can have antibacterial activity and therefore can be used in
                                                                                     Nucleic acids encoding useful for vaccinating
                                                                                                                            WPI; 2001-316495/33.
N-PSDB; AAH53764.
                                                                                                                                                                                                                     09-NOV-1999;
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                                                                                                                                                                                                                                                                       17-MAY-2001
                                                                                                                                                                                                                                                                                                WO200134809-A2
                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                   endocarditis
                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG82914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG82914 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated nucleic acid molecule from a Xanthomonas microorganism where the nucleic acid molecule is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule from a Xanthomonas microorganism, useful determining the presence of Xanthomonas bacteria in a sample.
                                                                                                                                                                                            (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                        epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                              2000WO-US030782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 52;
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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JF, De
                                                                                                                                                                                            GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                        open reading
                                                                                                                                                                                                                     99US-0164258P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC,
Laia
                                                                                     polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145pp;
                                                           2188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quaggio RB, Reinach FDC, F
ML, Setubal JC, Furlan LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696
                                                                                                                                                                                                                                                                                                                                                                                        frame protein sequence SEQ ID NO:2922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                cc them which are used to produce hosts cells which express the cc polypeptides. The polypeptides (II) (and/or nucleic acids) may then be cc used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the cc activity and therefore identify compounds that may be used for the cc polypeptides may also be used to assay for other inhibitors of their cc polynucleotide sequences from the present invention. AAH53971 to polynucleotide sequences and primers which are used in the cc represent oligonucleotide sequences and primers which are used in the cc exemplification of the present invention. N.B. The present invention cc specifically claims all the polynucleotide sequences given in the csequence listing of the present specification, however the sequence cc listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present corrected.
                                                 Matches
                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermidis polypeptides (II) via the production of vectors containing
  μ
                                                 7;
                                                                          Similarity
GPPGTKTXT 9
                                                                                                                                                696 AA;
                                               Conservative
                                                                        78.7%;
77.8%;
                                                                        Score 37; DB 4;
Pred. No. 1e+03;
                                                      Mismatches
                                                      2:
                                                                                              Length 696
                                                      Indels
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                                                      Gaps
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03-SEP-2001
                                                                     AAG81738;
                                                                                                    AAG81738 standard; protein; 715
epidermidis open reading
                                  (first entry)
frame protein sequence SEQ
   ID NO:570
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94

GEPGTKTIT 102

endocarditis. Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;

Staphylococcus

WO200134809-A2

09-NOV-2000; 2000WO-US030782

09-NOV-1999; 99US-0164258P

(GLAX) GLAXO GROUP LTD

Kimmerly

Nucleic acids encoding polypeptides from Staphylococcus epidermidis useful for vaccinating against infections, e.g. endocarditis. WPI; 2001-316495/33. N-PSDB; AAH52588.

Claim 18; Page 189; 2188pp; English

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the Ξ

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RESULT 13
ABP38222
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Best Local :
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55990 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6380370-B1
                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 3067; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-381255/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997;
08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-)
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gene therapy.
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97US-0064964P.
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77.8%;
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Pred. No. 1.1e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial infection;
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Query Match Best Local Similarity

78.7%; 77.8%;

Score 37; Pred. No.

DB 5; Length 846; 1.3e+03;

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GPPGTKTXT 9 GEPGIKTIT 102

Sequence 846

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AAG83
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                            AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present inverse which are used to AAH55098
                                                                                                                                                                                                                     represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316495/33.
N-PSDB; AAH53857.
                                                                                                                             Sequence 910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 819; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000; 2000WO-US030782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. epidermidis open reading frame protein sequence SEQ ID NO:3108
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                                 Local
                                                                                                                                                                                             SEQ ID NO:4455
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                              Similarity
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   Conservative
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                                 78.7%;
77.8%;
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                              Score 37; DB 4;
Pred. No. 1.3e+03;
   Mismatches
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                                                            Length 910;
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RESULT 15
ADS05211
ID ADS05
AC ADS06
AC
                                                                                                 CC given in the specification. Also described are: a recombinant expression CC given in the specification. Also described are: a recombinant expression CC vector; a cell comprising a recombinant expression vector of (1); CC producing an S. epidermidis polypeptide; an isolated nucleic acid CC comprising a nucleotide sequence of at least 8 nucleotides in length; a CC vaccine composition for prevention or treatment of an S. epidermidis CC infection, comprising a nucleic acid cited above and a carrier; treating CC preparation of an S. epidermidis infection; a recombinant or substantially CC pure preparation of an S. epidermidis polypeptide or its fragment; a CC vaccine composition for prevention or treatment of an S. epidermidis CC infection; detecting the presence of a Staphylococcus nucleic acid in a Sample; a computer readable medium having recorded in it the nucleotide CC system for identifying fragments of the Staphylococcus plasmids of commercial importance; a computer based system for identifying fragments of the Staphylococcus plasmids of commercial important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment CC of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment CC of the Staphylococcus genome and/or plasmids. The methods and CC infection. This is the amino acid sequence of a S. epidermidis bacterial infection. This is the amino acid sequence of a S. epidermidis protein of the staphylococcus provention and content of an Staphylococcus provention are useful for the diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1997;
13-AUG-1998;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
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                                                                                 invention.
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98US-00134001.
99US-00450969.
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Query Match 78.7 Best Local Similarity 77.8 Matches 7; Conservative

78.7%; 77.8%;

Score 37; DB 8; Length 997; Pred. No. 1.5e+03; Indels 0; Mismatches 2; Indels

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Sequence 997 AA;

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Search completed: April 18, Job time : 46.914 secs
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US-09-710-279-3108
US-09-710-279-3108
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US-09-138-092-1103
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                                                                               Sequence 1, Appli
Sequence 3068, Ap
Sequence 2344, Ap
Sequence 2638, Ap
Sequence 2496, Ap
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Sequence 570, App
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Sequence 3108, Ap
Sequence 1103, Ap
Sequence 1107, Ap
Sequence 1072, Ap
Sequence 19347, A
Sequence 1946, A
Sequence 14840, A
Sequence 14840, A
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US-09-134-001C-3069
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US-09-359-268A-1
Sequence 3069, Application US/09134001C

Sequence 3069, Application US/09134001C

Sequence 3069, Application US/09134001C

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PRIOR DATE: 1997-08-14
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Matches 9
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CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 199-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
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APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THERBOF
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TYPE: PRT
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                                                                ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3068
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                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
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SEQ ID NO 3069
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SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 2344
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                                                                                                                                                                                              FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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OTHER INFORMATION:
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TYPB: PRT
ORGANISM: Artificial Sequence
                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                ENGTH: 383
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77.8%;
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               78.7%;
77.8%;
Score 37; DB Pred. No. 1.5e
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Pred. No. 1.1e+02;
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                 DB 3;
1.5e+02;
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US-09-710-279-2638
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMI
FILE REFERENCE: BU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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Best Local S
Matches 7
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SEQ ID NO 2638
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Patent No. 6703492
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GENERAL INFORMATION:
                                                                   Matches
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Best Local :
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
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                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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TYPE: PRT
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                 TYPE: PRT
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LOCATION: (470)
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44 GEPGTKTIT 52
                                                               l Similarity
7; Conserva
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                                GPPGTKTXT 9
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                                                                                   78.7%;
77.8%;
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77.8%;
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Pred. No. 1.8e+02;
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Pred. No. 1.6e+02;
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                                                                     Mismatches
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RESULT 9
US-09-134-001C-3067
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US-09-710-279-570
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US-09-710-279-570
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US-09-710-279-2922
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APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
PILE REFERENCE: PU3480US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2922
                                                    GENERAL INFORMATION:
                                                                        Sequence 3067, Application US/09134001C Patent No. 6380370
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LENGTH: 715
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Best Local (
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Best Local
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Patent No. 670349
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NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 2.7e
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Pred. No.
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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3067
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-09-710-279-3108
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US-09-710-279-3108
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TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3067
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APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3108
1.PRICTEL 310
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3530
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APPLICANT: Lynn Dou
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Patent No. 6703492
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Best Local
                                   APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-10-08-14
PRIOR FILING DATE: 1997-08-14
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ORGANISM: Artificial Sequence
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Pred. No. 3.4e+02
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Pred. No. 3.2e+02;
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3530
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US-09-538-092-1103
                                                                                                        NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1072
                                                                                                                                                                                                                                                                                                                                                              Sequence 1072, Application US/09538092 Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P40937
-09-538-092-1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1103
                                                                                                                                                                                                                                                                                                                                    Patent No. 6753317
                                                                                                                                                                                             FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR PELING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: Giot, APPLICANT: Mans:
                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/178,965 PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Giot, APPLICANT: Mans
                                                    ORGANISM: Homo sapiens
                                                                                     LENGTH:
                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                       PPLICANT: Mansfield, Traci A.
AME/KEY: misc_feature
OCATION: (0)...(0)
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Local Similarity 77.8%;
les 7; Conservation
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Similarity 80.0%;
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Pred. No. 2.3e
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Pred. No. 4.4e+02;
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US-09-248-796A-19347
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SOFTWARE: PatentIn V
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                         Sequence 19347, Application US/09248796A Patent No. 6747137
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                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION UNMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                   APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                              NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                              FILE REFERENCE: 107196.13;
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                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: saccharomyces cerevisiae
                                                                                             ORGANISM: Candida albicans
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                            Score 35.5;
Pred. No. 66
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Pred. No. 2.
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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2005 Compugen Ltd.
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cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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36	37 36	37	37	37	37	4.0	Score
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US-10-408-765A-1776 US-10-108-260A-3237	US-10-282-122A-71232 US-10-425-114-57982	US-10-470-048B-296 US-10-172-502-19	US-10-418-861B-52 US-10-437-963-107474	US-10-767-701-44355 US-10-437-963-156740	US-10-424-599-176807	US-10-652-334-1	ID
Sequence 1776, Ap Sequence 3237, Ap	Sequence 71232, A Sequence 57982, A	Sequence 296, Appl Sequence 19, Appl	Sequence 52, Appl. Sequence 107474,	Sequence 156740,		Sequence 1, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15
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111	93	781	642	639	637	626	611	447	415	409	394	383	382	371	369	367	363	353	344	340	339	336	319	311	300	256	224	188	139	4455
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	-10-437-96	-437-96:	-10-425-11	-10-425-	-10-424-599-23350	-10-437-96	-10-369-493-10	-10-369-493-57	2-334-	-10-369-493-9	-10-369-493-	-10-425-114	-437-963-	-10-369-493	-10-369-493	-10-425-114-	-10-369-49	-10-369-493	-10	-10	US-10-437-963-176776	-10	-10-3	-10-3	US-10-767-701-38318	-10-	US-10-264-049-2364		-10-767-701-36	-10-287-226-30
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10, Appl	180141,	176775,	٠	37717, A	233501,	166322,	•	5790, Ap	25, Appl	955, App	13298, A	42743, A			18667, A	'n		22192, A	2	1941, Ap	176776,	210517,		12479, A	38318, A	145467,	2364, Ap	1880	659	

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US-10-652-334-1
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10652334
Publication No. US20040115787A1
GENERAL INFORMATION:
                                                                                          Query Match
Best Local (
                                                                          Matches
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
                                                                                                                                                                  ORGANISM: Saccharomyces cerevisiae FEATURE: OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                               LENGTH:
                                                                        Similarity
9; Conserv
                                    GPPGTKTXT 9
                                                                          Conservative
                                                                                          95.7%;
                                                                  0;
                                                                                          Score 45; DB 16;
; Pred. No. 1.3e+06;
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                                                                                                            Length 9;
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                                                                      Gaps
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RESULT 4
US-10-767-701-44355
; Sequence 44355, App
; Publication No. US
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LENGTH: 344
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 176807, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao Yongwei
TITLE OF INVENTION: SQU vucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FAPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_130674C.1.pep
                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
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LOCATION: (1)..(126)
OTHER INFORMATION: unsure at all Xaa locations
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TYPE: PRT
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Application US/10767701 US20040172684A1
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77.8%;
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85.7%;
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Pred. No. 1.6e+02;
l; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 156740
LENGTH: 563
                                                                                       Sequence 52, Application US/10418861B Publication No. US20040010131A1 GENERAL INFORMATION:
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Best Local Similarity 85.7%;
Matches 6; Conservative
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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Best Local
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               APPLICANT: da Silva, Ana Claudia Rasera
APPLICANT: Farah, Shaker Chuck
APPLICANT: Quaggio, Ronaldo Bento
APPLICANT: Reinach, Fernando de Castro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILS REFERENCE: 38-21(53221)B
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: SORBI-28MAY03-C2240_1.pep
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Wu, Wei
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Zhou, Yihua
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Barbazuk, Brad
Ferro,
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Jesus Aparecido
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75.0%;
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Pred. No. 5.4e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                      Score 37; DB 16;
Pred. No. 6.9e+02;
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FILE REPERENCE: FARESP 205.1 US
CURRENT APPLICATION NUMBER: US/10/418,861B
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/374,620
PRIOR PILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 52
LENGTH: 577
TYPE: PRT
ORGANISM: Xanthomonas
                                                     US-10-470-048B-296
Sequence 296, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
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-10-437-963-107474
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SEQ ID NO 107474
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APPLICANT:
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN FILE REFERENCE: SONN:035US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules,
TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 593
                                                                                                                                                                                                                                                                                                        Local
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Similarity 85.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                    Score 37; DB 16;
Pred. No. 7.3e+02;
1; Mismatches 0
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/470,048B;
CURRENT FILLING DATE: 2003-07-25;
NUMBER OF SEQ ID NOS: 603;
SOFTMARE: PatentIn version 3.1;
SEQ ID NO 296;
LENGTH: 1030;
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
FEATURE:
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US-10-172-502-19
; Sequence 19, Application US/10172502
; Publication No. US20030185833A1
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; TYPE: PRT
; ORGANIEM: Staphylococcus epidermidis
US-10-172-502-19
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US-10-282-122A-71232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/172,502
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/298,098
PRIOR FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                Sequence 71232, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITHA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOSTER, Timothy et al.
TITLE OF INVENTION: CROSS-REACTIVE MONOCLONAL AND POLYCLONAL ANTIBODIES.
FILE REFERENCE: P07263US01/BAS
                                                                                                                                                                                                                                          APPLICANT: Wang,
APPLICANT: Zamuc
                                                                                       APPLICANT:
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LOCATION: (269)...(271)
OTHER INFORMATION: X = anything
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7; Conserva
                                                                                   Yamamoto, R. Forsyth, R.
                                                                                                                                      Wall, Daniel
Trawick, John
                                                                                                                                                                         Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                             Haselbeck, Robert
                                                                                                                                                                                                                          Zamudio, Carlo
Malone, Cheryl
                                                                                                                      Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                       Robert
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77.8%;
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77.8%;
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Pred. No. 1.3e+03;
Pred. No. 1.3e+03;
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Pred. No. 1.
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                                                                                                                                     ; OTHER INFORMATION: US-10-425-114-57982
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Best Local Similarity
7; Conservation
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71232
                                                                                                                                                                                                                                          SEQ ID NO 57982
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                                                                   Matches
                                                                                                  Query Match
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                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                        LENGTH: 140
TYPE: PRT
                                                                                                                                                                       FEATURE:
                                                                                                                                                                                    ORGANISM: Zea mays subsp. mexicana
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                                                                                   Local
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/230,347
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 41 GPPGTK 46
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                                                                  Similarity 6; Conserv
                                 GPPGTK 6
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Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                               Cao, Yongwei
                                                                   Conservative
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77.8%;
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Pred. No. 2.9e+03;
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                                                                     Mismatches
                                                                                   DB 15; 1
2.5e+02;
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RESULT 12

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US-10-108-260A-3237
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                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3237
LENGTH: 1330
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US200400055
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Matches 6; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1776
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                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                         Sequence 2, Application US/10202167 Publication No. US20030143564A1
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: Keene, Douglas R.
APPLICANT: Brunken, William Joseph
TITLE OF INVENTION: COLLAGEN XXII, A
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 10287-072001
                                                                                    APPLICANT: Burgeson, Robert Eugene
APPLICANT: Koch, Manuel
APPLICANT: Bruckner-Tuderman, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ghosh, Soumitri
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ORGANISM: Homo sapiens
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6; Conserva
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                                                                                    Koch, Manuel
Bruckner-Tuderman, Leena
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Taylor, Steven W.
Glenn, Gary M.
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Pred. No.
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Pred. No.
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                                      A NOVEL HUMAN COLLAGEN
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RESULT 15
US-10-287-226-304
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-202-167-2
FILE REFERENCE: 21402-480C
CURRENT APPLICATION NUMBER: US/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,392
PRIOR PILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/360,148
PRIOR APPLICATION NUMBER: 60/360,148
PRIOR PILING DATE: 2002-02-27
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                          APPLICANT:
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CURRENT FILING DATE: 2003-03-31
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PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                        APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
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Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark B.,
Shenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
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MacDougall, John R.,
Mezes, Peter S.
Miller, Charles B.,
Millet, Isabelle,
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Chaudhuri, Amitabha,
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Boldog, Ference,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ellerman, Karen,
Gangolli, Esha A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khramtsov, Nikolai,
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Alsobrook, John P.,
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                                                                                                                                                                                                               Zerhusen, Bryan D.,
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Shlomit R.,
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PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 60/334,526
PRIOR FILING DATE: 2001-11-30
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PRIOR FILING DATE: 2001-11-28
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RESULT 1 T29836 hypothetical protein B0222.5 - Ca C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_rev C;Date: 15-Oct-1999 #sequence_rev		45 34.5						38 34.5								30 34.5
otein Buorhabdii 1999 #se		73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4	73.4
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- Caenorhabditis elegans ggans _revision 15-Oct-1999 #t	ALIGNMENTS	C86189	S23408	S62476	C84304	C84367	G85610	E90113	S34700	T42668	H64312	T41580	T28788	AD2086	B71420	AF2198
RESULT 1 T29836 hypothetical protein B0222.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T29836		protein T25N20.11	prematurely termin	hypothetical prote	DNA helicase [impo			hypothetical prote	probable purine nu	hypothetical prote	probable DNA helic	1	hypothetical prote			-

A;Residues: 1-369 <DUZ> A;Cross-references: UNIPROT:Q17457; EMBL:U50312; PIDN:AAA92322.1; CESP:B0222.5 A;Experimental source: strain Bristol N2 A; Description: The sequence of C. elegans cosmid BO: A; Reference number: Z20696 A; Raccession: T29836 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA 밁 S A; Gene: CESP: B0222.5 A; Introns: 27/2; 47/1; 86/1; 114/1; 158/1; 206/3; 244/1; 275/1; submitted to the EMBL Data Library, February 1996 A; Description: The sequence of C. elegans cosmid B0222. Matches Query Match Best Local 272 GPPGFKTTT 280 1 GPPGTKTXT 9 l Similarity 7; Conservat Conservative 83.0**%**; 77.8**%**; Score 39; DB; Pred. No. 18; 0; Mismatches 2; Length 369; 2 Indels 0; Gaps 0

RESULT 2

AH0631

hypothetical protein STY1143 [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0631 C;Pate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0631 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Dowd, L.; White, N.; Farrar, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Fitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serovi A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0631

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-312 <PAR>

A;Cross-references: C;Genetics: GB:AL513382; PIDN:CAD08235.1; PID:g16502282; GSPDB:GN00176

A;Gene: STY1143

Query Match

76.6%; Score 36; 띪 <u>ب</u> Length 312;

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F,429-431/Region: cell attachment (R-G-D) motif
F,447-449/Region: cell attachment (R-G-D) motif
F;147-449/Region: cell attachment (R-G-D) motif
F;1257-1259/Region: cell attachment (R-G-D) motif
F;1357-1380/Region: carboxyl-terminal nonhelical telopeptide
F;1357-1380/Region: carboxyl-terminal nonhelical telopeptide
F;1357-1380/Region: carboxyl-terminal nonhelical telopeptide
F;1403-1546/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #
F;1403-1546/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #
F;109-163,1511-1545/Disulfide bonds: #status predicted
F;319/Modified site: allysine (Lys) #status predicted
F;426,1266/Modified site: 5-hydroxylysine (Lys) #status predicted
F;426,1266/Modified site: 5-hydroxylysine (Lys) (covalent) #status experimental
F;942,1023,1299/Modified site: 5-hydroxylysine (Lys) #status experimental
F;942,1023,1299/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;4427,1433,1450,1459/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol F;1-254/Domain: non-collagenous (fragment) #status predicted <NC3>
F;1-189/Product: proline/arginine-rich PARP protein (fragment) #status predicted <PARP>
F;255-305/Domain: collagenous, triple helix #status predicted <COL2>
F;306-342/Domain: non-collagenous #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: structural component of extracellular fibrous polymer associated with A;Note: may play a role in controlling the lateral growth of collagen II fibrils C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:J04974; NID:g180714; PIDN:AAA52034.1; PID:g180715
A;Note: parts of this sequence were determined by protein sequencing
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:L18987; NID:g306439; PIDN:AAA35498.1; PID:g306440 R;Kimura, T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattei, M.G.; van der Rest, M.; J. Biol. Chem. 264, 13910-13916, 1989 A;Title: The human alpha2(XI) collagen (COL11A2) chain. Molecular cloning of cDNA and ge A;Reference number: A32645; MUID:89340485; PMID:2760050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A;Note: the list of introns is incomplete
C;Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:CGH 3(XI) chain (see PIR:CGHUGC), initially linked by disulfide bonds among their carboxyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Zhidkova, N.I.; Brewton, R.G.; Mayne, FEBS Lett. 326, 25-28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 2(XI) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;343-1356/Region: helical
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A; Residues: 586-1546 < KIM>
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A; Residues: 1-663 < ZHI>
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Date: 07-Jun-1990 #sequence_revision 03-Oct-1995
Accession: S34790; A32645
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Alternate names: procollagen alpha 2(XI)
Contains: proline/arginine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GDB:119788; OMIM:120290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S34790
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                                                              site: carbohydrate (Asn)
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   76.6%;
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1; Mismatches
   Score
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(XI) chain
   36;
                                                              (covalent)
   DB 1;
                                                              #status predicted
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   Length 1546;
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                                                                                                                            #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                    #status
                                                                                                                                                                                                                                                                                                                                                                                                              <CTP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ogawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S17231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dynein alpha
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F;154-161/Region: nucleotide-binding motif A (P-loop)
F;1852-1859/Region: nucleotide-binding motif A (P-loop)
F;2133-2140/Region: nucleotide-binding motif A (P-loop)
F;2460-2467/Region: nucleotide-binding motif A (P-loop)
F;2805-2812/Region: nucleotide-binding motif A (P-loop)
F;2805-2812/Region: nucleotide-binding motif A (P-loop)
F;160/Binding site: ATP (Lys) #status predicted
F;1658/Binding site: ATP (Lys) #status predicted
F;2466/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: Intron positions not resolved (incomplete sequence)
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;575-582/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Tittle: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain A;Reference number: Z16302; MUID:94274778; PMID:8006077
A;Accession: T08164
                                                                                                                                                                                                                                            A;Accession: PS0415
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 764-1001, 'APQ', 1005-2036, 'VPSSVET' <OG2>
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: ATP; heterotetramer; hydrolage; microtubule binding; nucleotide binding; P-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 352, 643-645, 1991
A;Title: Four ATP-binding sites in the midregion of the beta heavy chain of dynein.
A;Reference number: S17231; MUID:91326104; PMID:1830928
                                                                                                                                                                                                                                                                                                                                                                                 A; Title: ATP-binding site A; Reference number: PS0415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-4466 <OGA>
A;Cross-references: UNIPROT:P39057; GB:D01021; NID:g217202; PIDN:BAA00827.1; PID:g217203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Sep-1991 #sequence revision 02-May-1994 #text_change 09-Jul-2004 C;Accession: S17231; PS0415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Anthocidaris crassispina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dynein beta heavy chain, ciliary -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:L26049; NID:g415679; PIDN:AAA57316.1; PID:g603079
A;Experimental source: strain 21gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-2405 <MIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contains: dynein ATPase (EC 3.6.4.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
Matches
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         B Phys. Biol. Sci. 67, 27-31,
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                                                                                                                                                                                                                                                                                                                                                                                                                in dynein
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Pred. No.
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  beta-heavy
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1991
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: C69507
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F;1852-1859/Region: nucleotide-binding motif A (P-loop)
F;2133-2140/Region: nucleotide-binding motif A (P-loop)
F;2460-2467/Region: nucleotide-binding motif A (P-loop)
F;2805-2812/Region: nucleotide-binding motif A (P-loop)
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N;Contains: dynein ATPase (EC 3.6.4.2)
C;Species: Tripneustes gratilla
C;Date: 04-Dec-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: S17653; S24628
R;Gibbons, I.R.; Gibbons, B.H.; Mocz, G.; Asai, D.J.
Nature 352, 640-643, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 162-172;1193-1204;3240-3259;3325-3339 <GIB2>
C;Superfamily: dynein heavy chain, ciliary
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                                                C; Superfamily:
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A;Cross-references: UNIPROT:P23098; EMBL:X59603; NID:g10709; PIDN:CAA42170:1; PID:g10710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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                                                                                                 A;Residues:
                                                                                                                      A; Molecule type: DNA
                       ;Residues: 1-319 <KLB>
;Residues: 1-319 <KLB>
;Cross-references: UNIPROT:O28219; GB:AE000961; GB:AE000782; NID:g2689284; PIDN:AAB8919
;Superfamily: phage T4 DNA polymerase accessory protein 44
                                                                                                                                                                                                                                                                                                                                                                                                                ctivator 1, replication factor C, 35 KD subunit homolog - Archaeoglobus fulgidus
;Species: Archaeoglobus fulgidus
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                             Status: preliminary; nucleic acid sequence not shown; translation not shown
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Query Match
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2139/Binding site: ATP
2466/Binding site: ATP
2811/Binding site: ATP
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R;Li, X.; Burgers, P.M.J.

Proc. Natl. Acad. Sci. U.S.A. 91, 868-872, 1994
A;Title: Molecular cloning and expression of the Saccharomyces cerevisiae RFC3
A;Reference number: A36988; MUID:94134732; PMID:8302859
A;Accession: A36988
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C;Accession: B86350

C;Accession: B86350

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. Alber, M.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                   R;Cullmann, G.; Fien, K.; Kobayashi, R.; Stillman, B. Mol. Cell. Biol. 15, 4661-4671, 1995
A;Title: Characterization of the five replication factor C A;Reference number: S59664; MUID:95379808; PMID:7651383
A;Accession: S59666
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-340 <LIA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 25-Aug-1995 #sequence revision 25-Aug-1995 #text_change
C;Accession: A36988; S59666; S60412; S63264; S63266; S44762
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C; Superfamily: 1
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C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Residues: 1-319 <STO>
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;Title: Sequence analysis of a 30 kb DNA segment from yeast C, and a novel putative serine/threonine protein kinase gene;Reference number: S60394; MUID:96132033; PMID:8553702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Saccharomyces cerevisiae
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R; Nojima, H.
submitted to the EMBL Data Library, August 1998
A; Bescription: CDNA of rfc3.
A; Reference number: Z22496
A; Accession: T43412
A; Accession: T43412
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
R;Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B.; Pierard, A.; Glansdorff, submitted to the Protein Sequence Database, April 1996
                                                                                                                                                       A;Cross-references: EMBL:AB017040; PIDN:BAA82746.1
R;Gray, F.C.; MacNeill, S.A.
submitted to the EMBL Data Library, November 1998
A;Description: Characterisation of the rfc3+ gene
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A;Residues: 1-340 <MAW>
A;Residues: 1-340 <MAW>
A;Cross-references: EMBL:Z71566; NID:g1302374; PIDN:CAA96207.1; PID:g1302375; GSPDB:GN0d
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A;Cross-references: EMBL:Z71566; NID:gl302374; PIDN:CAA96207.1; PID:gl302375; GSPDB:GN00
A;Experimental source: strain S288C
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A; Accession: S63264
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A; Residues: 1-340 < MAU>
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                                                                                                       A;Reference number: Z22600
A;Accession: T43651
                                                     A;Residues:
                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-342 < NO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replication factor C chain Rfc3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:RFC3; MIPS:YNL290w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S63266
A;Accession: S63266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description: the RPC complex functions as a structure-specific, DN Note: each of the five chains are essential for cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Cross-references: SGD:S0005234; MIPS:YNL290w
;Map position: 14L
;Complex: heteropentamer consists of RFC1 (PIR:S44763), RFC2 (PIR:S45531), RFC3 (PIR:A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description: Rfc3 of S.p. Reference number: Z22494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA Residues: 1-342 <NOJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Schizosaccharomyces pombe;Deties: Schizosaccharomyces pombe;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004;Accession: T43410; T43412; T43651; T38458
Cross-references: EMBL:AJ012839; PIDN:CAB38106.1
Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:014003; EMBL:AB017039; PIDN:BAA82745.1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: phage T4 DNA polymerase accessory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPPGT-KTXT 9
                                                  1-342 <GRA>
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8; Conserva
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Pred. No. 70;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        August 1998
                                                                                                                                                             rfc3+ gene encoding a subunit of replication fact
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M.A.; Wood,
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C;Date:
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 119-342 <MUR>
A;Cross-references: EMBL:Z98978; PIDN:CAB39134.1; GSPDB:GN00066; SPDB:SPAC27E2.10c
A;Experimental source: strain 972h-; cosmid c27E2
C;Genetics:
A;Map position: 10R
C;Superfamily: phage T4 DNA polymerase accessory
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cullmann, G.; Fien, K.; Kobayashi, Ř.; Stiliman, B. Mol. Cell. Biol. 15, 4661-4671, 1995
A;Title: Characterization of the five replication factor A;Reference number: S59664; MUID:95379808; PMID:7651383
A;Accession: S59665
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A;Introns: 25/2; 47/1; 118/2; 143/1; 267/1
C;Superfamily: phage T4 DNA polymerase acc
                                                                                                                                                                                     A;Cross-references: EMBL:L47993; NID:g1019675; PIDN:AAB39294.1; PID:g1019690 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Octo
                                                                                                                                                                                                                                                                                                                         R;Huang, M.B.; Manus, V.; Chuat, J.C.; Galibert, F.
Yeast 12, 869-875, 1996
A;Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36
A;Reference number: S71676; MUID:96437976; PMID:8840504
A;Accession: S71690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P40348; EMBL:D28499; NID:g498462; R;Manus, V.; Huang, M.E.; Gallbert, F. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The RFC2 gene encoding a subunit of replication A;Reference number: S45531; MUID:94261414; PMID:8202350 A;Accession: S45531
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C;Species: Saccharomyces cerevisiae
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                                                                            A;Cross-references:
A;Map position: 10R
                                                                                                                             A; Gene: SGD: RFC2
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A; Residues: 55-71; 187-190; 296-315 < CUW >
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A;Accession: S59979
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A; Residues: 1-353 < CUL>
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R;Cullmann, G.; Fien, K.; Kobayashi, R.; Stillman, B.
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A; Residues: 1-353 < MAN>
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Nucleic Acids Res. 22, 1527-1535, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J1808; protein YJR068w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown
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                                                                                                      SGD:S0003829; MIPS:YJR068w
                                                                                                                                                                                                                                                                                                                                                                                                                                     V.; Chuat, J.C.; Galibert,
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Pred. No. 7:
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RESULT 14
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A45253
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84356
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Proc. Natl. Acad. Sci. U.S.A. 89, 5211-5215, 1992
A;Title: Studies of the cloned 37-kDa subunit of activator 1
A;Reference number: A45253; MUID:92302215; PMID:1351677
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                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-369 <STO>
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A;Residues: 1-363 <CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted
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;Residues: 65-83;94-101;125-134;147-163;261-272 <CH2>
                                                                                                                                                                                                                                                                                                                                      ;Status: preliminary
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;Species: Homo sapiens (man)
;Oate: 31-Dec-1993 #secounce_revision 31-Dec-1993 #text_change 21-Aug-1998
                                                                                                                                                                                                                         Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type
                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:Q9HNK6; GB:AE004437; NID:g10581481; PIDN:AAG20214.1;
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Best Local :
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8; Conserv
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80.0%;
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                                                                                                                                                                   Score 35.5;
Pred. No. 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.5;
Pred. No. 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.5;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
R.; Danson, M.J.; Hough, D.W.; Maddocks, D.
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Search completed: April 18, Job time : 10.6715 secs

2005,

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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69309
                                                                                                                                                                                                                 A;Cross-references: UNIPROT:029773; GB:AE001071; GB:AE000782; NID:g2689394; PIDN:AAB9076. C;Superfamily: ATP-dependent 265 proteinase; FtsH/SEC18/CDC48-type ATP-binding domain how C;Keywords: ATP; nucleotide binding; P-loop F;178-382/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP> F;205-212/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408, 816-820, 2000

A;Authors: Huntet, J. Li, Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96804
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-409 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATPase AAA homolog - Archaeoglobus fulgidus
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C; Superfamily: phage T4 DNA polymerase accessory protein
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A;Molecule type: DNA
A;Residues: 1-369 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: A96804
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Best Local S
Matches 8
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205
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  214
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                                                                                                             Score 35.5; I
Pred. No. 85;
0; Mismatches
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; Dewar, K.;
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                        Score
 Query
Match
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47
                                                                                                                                                                                                                                                                                                                                               UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
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122.648 Million cell updates/sec
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 GPPGTKTXT 9
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                       Length DB
Q6H3Z9
Q8PKQ1
Q9LGA3
TERT_CANFA
Q684M7
Q9L470
PLS_STAEP
Q6UV38
Q9U231
Q9D231
Q9D231
Q9SE14
Q8ZQ44
Q8ZQ44
Q8ZQ44
Q8ZQ45
Q6UP2
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Q9D33
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Q9L1A0
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 CA2B_HUMAN
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017457 caenorhabdi
0911a0 streptomyce
07uaki shigella fl
083ih9 shigella fl
083ih4 tropheryma
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083ih4 tropheryma
083ih4 tropheryma
085ih2 oryza sativ
06b32 oryza sativ
06b323 mus crofa
091470 staphylococ
06uv37 staphylococ
06uv37 staphylococ
06uv37 staphylococ
09d231 mus musculu
07sel4 neurospora
08c7p6 salmonella
08zq44 salmonella
08zq46 salmonella
08ijp9 drosophila
09id5 gallus gall
07njp2 gloeobacter
096jf7 homo sapien
06c050 yarrowia li
08cBr3 mus musculu
097033 ephydatia f
06mgb2 rattus norv
08nfw1 homo sapien
069z23 mus musculu
0913442 homo sapien
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45	44	3	2	41	6	39	38	37	36	35	34	ü	32
35.5	35.5	35.5	35.5	35.5	36	36	36	36	36	36	36	36	36
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329	326	319	319	202	4511	4499	4488	4466	4466	1863	1860	1827	1736
N	N	N	μ	N	N	۳	N	۳	-	N	N	N	μ
Q6CNE4	Q8QNA5	Q9XI09	RFCS_ARCFU	Q7T2C9	Q7PXZ5	DYHA CHLRB	Q71JD2	DYHC_TRIGR	DYHC ANTCR	Q7Z3L5	Q8IZC6	QBUUMS	CA2B_MOUSE
Q6cne4 kluyveromyc	Q8qna5 ectocarpus	Q9xi09 arabidopsis	O28219 archaeoglob	Q7t2c9 brachydanio	Q7pxz5 anopheles g	Q39610 chlamydomon	Q71jd2 drosophila		P39057 anthocidari	Q7z3l5 homo sapien	Q8izc6 homo sapien	Q8uum5 oryzias lat	Q64739 mus musculu

ALIGNMENTS

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RESULT 3
Q7UAK1
ID Q7UA
AC Q7UA
DT 01-C
DT 01-C
DT 01-Hypo
GN Orde
OS Shig
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Q7UAK1;
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01-OCT-2003
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Q9L1A0;
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00280; BPTI_KUNITZ_1; UNKNOWN_1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
PROSITE; PS00484; THYRŌGLOBULIN_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 369 AA; 41135 MW; BEDDE119BB9969
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                          Hypothetical protein.
OrderedLocusNames=S4646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
STRAIN=A3(2) / M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=SC10G8.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative acetyltransferase.
                                                                                                                                                                                                                                                                                    113
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SM00211; TY;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  flexneri.
                                                                                                                                                                                                                                                                                                                                   GPPGTKT 7
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                                                                  (TrEMBLrel.
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77.8%;
                                                                    Last sequence update)
Last annotation update)
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Pred. No. 1.5e
1; Mismatches
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Pred. No. 1.5e+02;
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1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 264;
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Best Local S
Matches 6
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Best Local
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EMBL; AE016993; AAP19570.1; -
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; Lactamase_B; 1.
Hypothetical protein.
SEQUENCE 255 AA; 27898 MW; 9CBA06FBC1E6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q83IH9;
Q83IH9;
01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566; Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein SF4376.
                                                                                                                                                                                                     Pfam; PF00753; Lactamase B; 1.
Complete proteome; Hypothetical
SEQUENCE 276 AA; 30087 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=SF4376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                     EMBL; AE015443; AAN45792.1; -.
InterPro; IPR001279; Blactmase-like.
                                                                                                                                                                                                                                                                                                                                         through comparison with genomes of Escherichia Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella flexneri.
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DOI=10.1128/IAI.71
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[1]
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Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                'Genome sequence of Shigella flexneri 2a:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TaxID=623
92
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                                                                                                  6; Conserv
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GPPGTRAMT 100
                                                                                                     Conservative
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1.5.2775-2786.2003;
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66.7%;
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66.7%;
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Last annotation update)
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Pred. No. 2.2e+02;
                                                                                                                           Score 37;
Pred. No.
                                                                                                                                                                                                              grotein.
8C1F192E049E1145 CRC64;
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                                                                                                     Mismatches
                                                                                                2.4e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                          insights into pathogenicity ichia coli K12 and O157.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomics of Shigella
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RESULT 5 Q83IE3 ID Q83I

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Q83N44;
Q83N44;
O1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-MR-2004 (TrEMBLrel. 26, Last annotation update)
Iron (III) dicitrate ABC transporter substrate-binding protein.
Name=fecB; OrderedLocusNames=TWTO56;
Tropheryma whipple1 (strain Twist) (Whipple's bacillus).
Tropheryma whipple1 (strain Twist) (Whipple's bacillus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22495039; PubMed=12606174; DOI=10.1016/S0140-6736(03)12597-4; Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A., Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.R., von Herbay A., Goble A., Rutter S., Squares R., Squares S., von Herbay A., Farkhill J., Relman D.A.; Squares S., Squa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 13:1800-1809(2003).

GENOME RES. 13:1800-1809(2003).

EMBL; AE016850; AA044153.1; -.

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006827; P:high affinity iron ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
Putative iron-siderophore binding lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduced genome."
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ייבייניטטר TaxID=203267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 323 AA;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=TW066;
                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with
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146
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                                                                                                                                                                                   Similarity 6; Conserv
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GPPGTKS 152
                                                                                       GPPGTKT 7
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                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            35377 MW;
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85.7%;
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85.7%;
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                                                                                                                                                                                                                                       Score 37; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert C.,
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                                                                                                                                                                                                                                                                                                                                                                                            DF43ED97A3F11FCD CRC64;
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RESULT 7

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Q88AM5;
01-JUN-2003
                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Putative endo-beta-1.4-glucanase.
Name=OSJNOa018M17.6; Synonyms=B1339H09.3;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6H3Z9;
Sasaki T., Matsumoto T., Katayose Y.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ d EMBL; APO07149; BAD26550.1; -. EMBL; APO06453; BAD26493.1; -. GO; GO:0004553; F:hydrolase activity, hydrolyzi GO; GO:0005975; P:carbohydrate metabolism; IEA.
                                                                                                                                                                      SEQUENCE FROM N.A.
Sasaki T., Matsumo
Submitted (JUN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GG; GG:0005215; F:transporter activity; IEA
GG; GG:0006810; P:transport; IEA.
InterPro; IPR066059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria;
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OrderedLocusNames=PSPTO0364;
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                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47925 MW; 9EA429C47F88EB66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.7%;
75.0%;
                                                                                                                                                                        T., Katayose Y.; to the EMBL/GenBank/DDBJ
                                                                               Katayose Y.;
:he EMBL/GenBank/DDBJ databases
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Last annotation update)
plasmic sugar-binding pr
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Pred. No. 3.
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                         O-glycosyl .
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RESULT 10
Q91GA3
ID Q91GA
AC Q91GA
DT 01-OC
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RC STRAIN=306 / ATCC 13902 / XV 101;

RM MEDLINE=22022145; PubMed=12024211; DOI=10.1038/417459a;

RM MEDLINE=22022145; PubMed=12024211; DOI=10.1038/417459a;

RM da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Camarottte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Perreira R.C.C., Perro M.I.T.,

RA Paria J.B., Perreira A.J.S., Perreira R.C.C., Perro M.I.T.,

RA Pormighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Meidanis J., Menck C.F.M., Myacki C.Y., Moon D.H.,

RA Martins B.C., Meidanis J., Menck C.F.M., Myacki C.Y., Moon D.H.,

RA Martins B.C., Meidanis J., Menck C.F.M., Myaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Spinola L.A.F., Taskita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Comarcian G.F., Takita M.G., Telifi D., Tsai S.M., White F.F.,
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Best Local
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Q9LGA3;
Q9LGA3;
01-OCT-2000
01-OCT-2002
01-OCT-2002
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InterPro; IPR008928; Glyco_trans_6hp.
Pfam; PF00759; Glyco_hydro_9; 1.
PROSITE; PS00552; GLYCOSYL_HYDROL_F9_1; 1.
SEQUENCE 532 AA; 58570 MW; 594D747ClA4EDDE8 CRC64;
ESTs D22655(C0749).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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01-OCT-2002
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EMBL; AE011847; AAM36971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=92829;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Pred. No.
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RESULT 11
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Q6A548;
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25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhong H., Iwama H., Endo T., Ito H., F
Yano M., Jiang J., Gojobori T.;
"The genome sequence and structure of
Nature 420:312-316 (2002).
EMBL; AP002538; BAB03379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                Gene
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Mammalia; Eutheria; Carnivora;
MCBI_TaxID=9615;
                                                                                               -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: Belongs to the reverse transcriptase fan Telomerase subfamily.
-i- SIMILARITY: Contains 1 reverse transcriptase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
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Ehrhartoideae; Oryzeae; Oryza.
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                       Nasir L., Gault B., Campbell S., Veeramalai M., Gilbert D., MCFarlane R., Munro A., Argyle D.J.; "Isolation and expression of the reverse transcriptase component the Canis familiaris telomerase ribonucleoprotein (dogTERT).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15225880; DOI
Nasir L., Gault E.,
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                                                                                                                                                                                            the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme. SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TEP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PINX1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Telomerase is a ribonucleoprotein enzyme essential
                                                                                                                                                                                                                                                                                                                                                                                                336:105-113(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1016/j.gene.2004.03.
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Kanamori H.,
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q2.1.";
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MEDLINE=98343959; PubMed=9677330;

MEDLINE=98343959; PubMed=9677330;

Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;

Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;

Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;

Sullivan M., Houslay M.D.;

Sullivan M.S., Houslay M.D.;

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Q684M7;
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PROSITE; PS50878; RT POL; 1.

DNA-binding; Nuclear protein; Ribonucleoprotein;

RNA-directed DNA polymerase; Telomere; Transferase.

DOMAIN 595 926 Reverse transcriptase.
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Leeb T., Martins-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rena G., Begg F., Ross A., MacKenzie C., McPhee I. Huston E., Sullivan M., Houslay M.D.; "Molecular cloning, genomic positioning, promoter characterization of the novel cyclic amp-specific
                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                         EMBL;
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                               InterPro; IPR000299; Band_4.1. InterPro; IPR009127; JAK.
                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                               similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                               GO:0016301; F:kinase activity;
                                                                                                                                                                                                                                                                                                                           subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmacol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 5
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j IPR011009; Kinase_like.
j IPR009131; Nonrecepttyrkins.
j IPR000719; Prot kinase.
j IPR002290; Ser_thr_pkinase.
j IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPGTKTXT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martine-Wess P., Kuiper H., Distl
ar characterization of the porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGTRPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59:996-1011 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124823 MW; F5F55D791106C1A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107:103-107(2004).
kinase of the non-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,
28,
                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                            Tyr family of
                                                                                                                                                                                                                                                                  IBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muller M.;
2 gene on S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I., Campbell L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification, as phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                kinases. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSC 2q1.3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 13
Q9L470
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                                                                                                                                                                                                                   CC -1- SUDMILLURAR LOCATION: Attached to the cell wall peptidoglycan by CC an amide bond (By similarity).

REMBI; AJ249487; CAB77251.1; -.

DR GO; GO:0009986; C:cell surface; IEA.

GO; GO:0005618; C:cell surface; IEA.

RO; GO:0005737; C:cytoplasm; IEA.

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016020; C:membrane; IEA.

RO; GO:0016017; P:phosphate transport; IEA.

RO; GO:000617; P:phosphate transport; IEA.

RINterPro; IPR008161; Collagen.

InterPro; IPR008161; Collagen.

RINterPro; IPR00829; Csurface antigen.

RINterPro; IPR00829; CSurface antigen.

RINterPro; IPR00189; G5.

RINTERPAMS; TIGR01167; YSIRK signal; 1.

REGIONALS; CSURFACE antigen; 2.

RINTERPAMS; TIGR01168; YSIRK signal; 1.

REGIONALS; CSURFACE antigen; 2.

REGIONALS; CSURFACE ANTIGEN; 2.

REGIONALS; RESURAN, POS ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 6
Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
Cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00220; S_TKC; 2.

SMART; SM00219; TYRC; 2.

SMART; SM00219; TYRC; 2.

PROSITE; PSS0057; PERM 3; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 2.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Kinase; SH2 domain; Transferase; Tyrosine-protein kinase.

SEQUENCE 1184 AA; 132309 MW; 947255CC320B040B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hussain Shaikh M., Heilmann C., Peters G., Herrmann M.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00295; B41; 1.
SMART; SM00252; SH2; 1.
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF00069; Pkinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1282;
                                                                                                                                                                                                 wall; Peptidoglycan-anchor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPPGTKT 7
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PD000001; Prot_kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR01823; JANUSKINASE. PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGTET 133
                                                                                                                     1245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                            1245
                                                                                                                  52 Potential.
45 accumulation-associated protein.
131966 MW; B68425AAE45604D3 CRC64;
                             78.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.7%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                Score 37; DB 2;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
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                                                          Length 1245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Similarity 7; Conser

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Query Match
Best Local Similarity
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PLS STAI
QBCQD9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228)."; Mol. Microbiol. 49:1577-1593 (2003).

-i- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by the control of the cell wall peptidoglycan by the control of the cell wall peptidoglycan by the cell wall peptidoglycan by
                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
TIGRFAMS; TIGR01168; YSIRK_signal; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00746; Gram pog_anchor; 1.
Pfam; PF04650; YSJRK signal; 1.
Probom; PD0000007; Clg helix; 2.
Probom; PD153432; Csurface_antigen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=SE0175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (Rel.
05-JUL-2004 (Rel.
05-JUL-2004 (Rel.
                                                                  SEQUENCE
                                                                                                          MOD_RES
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     Cell wall; Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF07501; G5; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005877; Gpos_YSIRK.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE016744; AAO03772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an amide bond (rotential).
-!- SIMILARITY: Contains 7 G5 repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accumulation-associated protein precursor.
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004829; Csurface_antigen.
InterPro; IPR011098; G5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008160; Collagen.
InterPro; IPR008985; ConA_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amide bond (Potential)
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1436
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Pentaglycyl murein |
threonine (Potentia
                                                                                                                                                           Score 37; DB 1;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                     Accumulation-associated protein. Removed by sortase (Potential).
                                                                                                                                                                                                                                                                                                                                                                  Peptidoglycan-anchor; Repeat; Signal. Potential.
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urein peptidoglycan
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RESULT 15
Q6UV37
Search completed: April 18, 2005, 08:15:36
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                                                                                                                                                                                                                                           Matches
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Pfam; PF07501; G5; 6.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF004650; YSIRK signal; 1.
Pfam; PF004650; YSIRK signal; 1.
ProDom; PD153432; Csurface antigen; 2.
TIGRPAMs; TIGR01167; LPXTG_anchor; 1.
TIGRPAMs; TIGR01168; YSIRK signal; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
Ccell wall; Peptidoglycan-anchor.
Ccell wall; Peptidoglycan-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an amide bond (By similarity).

EMBL; AY359816; AAQ83699.1; -.

GO; GO:000986; C:cell surface; IEA.

GO; GO:0005618; C:cell wall; IEA.

GO; GO:0005737; C:cyroplasm; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0006817; P:phosphate transport;

GO; GO:0006817; P:phosphate
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rohde H., Mack D.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Gapop 10.0 , Gapext 0.5
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57
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 A_Geneseq_16Dec04:*
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                  ADP23318
AAM80260
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AAAO17597
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AAV77815
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Aay77805 Motif II
Aay77814 Yeast Upf
Abw01205 Saccharom
Adp44131 Yeast hel
Ads21255 Bacterial
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ntacting modulator of translation termination (Mtt1) is cerevisiae with a test agent, and detecting specific 1. 1 41-42; Opp; English. relates to a method of identifying an agent that incre	; 2003-810549/76. ntifving an agent that increases nonsense suppression, for ant	Peltz S, Czaplinski K, Dinman JD;	NB-) UNIV NEW JERSEY M	22-JUL-1998; 98US-0093685P.	22-UUL-1999; 99US-00359268.	07-OCT-2003.	630294-B1.	/arrerence		c-difference	Key Misc-difference 4	Saccharomyces cerevisiae.	Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast.	Saccharomyces cerevisiae motif II peptide.	15-JAN-2004 (first entry)	ABW01178;	W01178 ABW01178 ståndard; peptide; 14 AA.	ALIGNMENTS	5 34.5 60.5 1187 4 AAU07865 Aau07865 Polype	3 34.5 60.5 III8 6 ABG/3900 ABG/3900 4 34.5 60.5 1140 2 AAY21377 ABY21377	2 34.5 60.5 1043 2 AAW36509 Aaw36509	0 34.5 60.5 935 7 ADJ69900 Adj69900	9 34.5 60.5 925 8 ADN19434 Adn19434	7 34.5 60.5 550 6 ABB99781 Abb99781	5 35 61.4 658 8 ADQ59484 Adq59484 6 34.5 60.5 517 6 ABB99784 Abb99784	4 35.5 62.3 1944 8 ADN19868 Adn19868	2 35.5 62.3 988 6 AACC6745	0 35.5 62.3 685 4 ABB58231 Abb58231	8 36.5 64.0 2000 7 ADK64622 9 36.5 64.0 2231 8 ADN19177 Adn19177	26 36.5 64.0 1417 4 ABB63329 ADD63329 DIGBEORITE 27 36.5 64.0 2000 6 ABR53451 Abr53451 Protein s	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia B; Haemophilia B; Souther Dystrophy; Haemophilia B; Haemophilia B; Souther Berast Cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast Cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; translation termination; RNA helicase; MTT1;
frameshift frequency; aberrant transcript degradation;
                                                                                                                                                                                                                                                                                                                                                                                                         (CZAP/)
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22-JUL-1999;
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                                                            Claim 34;
                                                                                                                     composition or agent, and inhibits the MTT1.
                                                                                                                                             Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                  WPI; 2004-449400/42.
                                                                                                                                                                                                                                                                                                                           Peltz S,
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CZAPLINSKI K.
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                                                            SEQ ID NO 2; 41pp; English
                                                                                                                                                                                                                                                                                                                     Czaplinski K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0093685P
99US-00359268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 termination modulation protein motif II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Any amino acid"
                                                                                                                                                                                                                                                                                                                           Dinman JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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0.0022;
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The invention

relates to a method of identifying a test composition that

Claim 34; Page 79; 89pp; English.

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RESULT 3
AAY77805
ID AAY7
XX AAY7
XX AAY7
XX AAY7
XX Moti
XX Heli
XX Heli
XX Heli
XX Unid
XX Unid
XX Unid
XX Unid
XX EFF Misc
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CC permitting binding between the MTII and the composition, detecting
CC specific binding of the test composition or agent to the MTII. The
CC determining if the test composition or agent to the MTII. The
CC composition and methods are useful for modulating the fidelity of
CC translation termination or for identifying agents that: affect the
CC translation activity of mRNAs by altering frameshift frequency, permit
CC monitoring of a termination event, promote degradation of aberrant
CC transcripts, and provide modulators (inhibitors/stimulators) of peptidyl
CC transferase activity during initiation, elongation, termination and mRNA
CC degradation of translation. The agents, which may be antagonists or
CC agonists, are useful in screening, diagnostic and therapeutic purposes,
CC for diseases or conditions resulting from or cause premature translation,
CC such as beta-thalassaemia, beta-globin, buchemne/Becker Muscular
CC pystrophy, Haemophilia A, Haemophilia B, Von Willebrand Disease,
CC Hirschsprung disease, Cystic fibrosis, Kidney Stones, Familial
CC hypercholesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis,
CC the amino acid sequence of the yeast translation termination modulation
CC profesis mortif II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                     New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Motif II comprised in a gene modulating translation termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY77805 standard;
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                                                                                                                                                                                            WPI; 2000-171458/15.
                                                                                                                                                                                                                                                                Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                (UYNE-) UNIV NEW JERSEY
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                                                                                                                                                                                                                                                                Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                98US-00120435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US016802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "reisdues indicated Xaa are unspecified"
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                                                                                                                                                                                                                                                                   Dinman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ጅ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Lo. 0.0022; ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
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CC transferase activity, especially diseases resulting from a nonsense or compensation e.g. beta-thalassemia, beta-globin, Duchene/Becker CC frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker CC involving a defect in the complex, by transferting cells with encoding cc and after transferase activity disease conditions complex of defective complex before cc and after transferase activity during translation, inhibiting the peptidyl transferase activity during translation, inhibiting the complex expression and so modulate the efficiency of interaction between MTI and eRE3 or involved in enhancing translation cc termination. Vectors comprising polynucleotides encoding the complex (or contribute equation) and so modulate the efficiency of contributes in a cell. Agents binding to the complex can be identified complex capteression and so modulate the efficiency of combinate peptidyl transferase activity during translation in cells. They care also useful to modulate the efficiency of translation of aberrant cc are also useful to modulate the efficiency of translation of aberrant cc compositions modulate the efficiency of translation facels. They care also useful to modulate the efficiency of translation of aberrant cc compositions modulate the efficiency of translation termination of compositions modulating binding to MTI, useful to identify agents of interact. used for modulating ranslation facels in the genes of interact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast Upf1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY77814 standard; peptide; 380 AA
  WPI; 2000-171458/15
                                                   Peltz S,
                                                                                                                                                                                                            22-JUL-1999;
                                                                                                                                                                                                                                                                   03-FEB-2000.
                                                                                                          (-BNYU)
                                                                                                                                                           22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            helicase; Upfl.
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                                                   Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein fragment.
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                                                                                                          NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for modulating
                                                                                                                                                           98US-00120435
                                                                                                                                                                                                               99WO-US016802.
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100.0%; Pred. No. 0.
Live 0; Mismatches
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                                                         Dinman
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밁 S

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CC Muscular Dystrophy etc. It can be used to identify disease conditions (CC Muscular Dystrophy etc. It can be used to identify disease conditions (CC involving a defect in the complex, by transfecting cells with encoding (CC nucleic acid and determining the proportion of defective complex before (CC and after transferase activity during translation, inhibiting the (CC interaction between MTT) and eRF3 or involved in enhancing translation (CC entities esquences) can be constructed and introduced into cells to (CC antisense sequences) can be constructed and introduced into cells to (CC interfere with complex expression and so modulate the efficiency of (CC translation termination of mRNA and/or degradation of aberrant (CC translation therapeutic compositions useful as above, and/or used to (CC and included in therapeutic compositions useful as above, and/or used to (CC and included in therapeutic compositions useful as above, and/or used to (CC as a lso useful to modulate the efficiency of translation in cells. They (CC are also useful to modulate the efficiency of translation termination of (CC mRNA) at a nonsense codon and/or promote degradation of aberrant (CC compositions modulating binding to MTT1, useful to identify agents) (CC Sequences ANY77813-817 represent protein fragments from yeast superfamily)
Translation Termination, and the control cells, peptidyl carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulate peptidyl transferase activity during translation in a cell. can be administered therapeutically combined with a carrier in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a new multiprotein complex which can modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 89pp; English.
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밁 S Matches Query Match Local 31 1 RILXCA-SNXAVDXL 14 11; Conservative Similarity RILVCAPSNVAVDHL 45 71.1%; Score 40.5; D Pred. No. 10; 0; Mismatches 0; DB 3; 'n Length 380; Indels ۲. Gaps ۲

Sequence 380 AA;

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RESULT 5
ABW01205
ID ABW0
XX ABW0
XX ABW0
XX ABW0
XX Sacc
XX Sacc
XX Modu
KW Modu
KW thez
XX US66
                                                                                                                                                                                                                                                  22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulator of translation termination; MTT1; helicase B; therapy; HCSB; nonsense mutation; yeast; RENT1; HUPP1; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae UPF1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABW01205 standard; protein; 380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerevisiae
                                                                                                                                                                                                                                                         9908-00359268
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в; antiviral; ; UPF1.

22-JUL-1998;

98US-0093685P

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

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RRESULT 6
RDP44131
ID ADDP44
XX ADDP4
XX ADDP4
XX YOAR
DT 18-N
XX YOAR
XX YOAR
XX YOAR
XX YOAR
XX YOAR
XX OVAT
XX OVAT
XX NEUT
XX SACC
YN US20
XX I17-J
XX 28-J
PF 28-J
XX 28-J
PF 28-J
XX (PEI
PA (CZJ
PA (DEI
PA (CZJ
PA (DEI
PA (DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; translation termination; RNA helicase; MTT1; frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterclaemia; Retinitis Pigmentosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae UPF1 (otherwise termed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mttl.
Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP44131 standard; protein; 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast helicase
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                                                                                                                                                                             Peltz S,
                                                                                                                                                                                                                                    (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
(DINM/) DINMAN J D.
                                                                                                                                                                                                                                                                                                                                                        22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2003; 2003US-00652334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurofibromatosis; Retinoblastoma;
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                                                                                                                                                                          Czaplinski K,
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99US-00359268.
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73.3%;
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Pred. No. 10;
0; Mismatches
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RRESULT 7
ADS21252
XX ADS22
XX ADS2
XX Pactor
DT 02-D
DT 02-D
XX Recold
KW Recold
KW Path
KW bact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth repulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                                                                                      (HINK/)
(SLAT/)
(CHEN/)
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   Cao Y,
                                                                                                                                                                                                                                       21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial polypeptide #10288.
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                                                                                                                                                                                  (CAOY/)
                                                          (GOLD/)
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                                                                                            HINKLE G
SLATER S
CHEN X.
                                                          CHEN X.
GOLDMAN B
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   Hinkle GJ,
                                                                                                                                                                                  CAO Y.
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                                                                                                                 G.
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   Slater SC,
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73.3%;
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Pred. No. 10;
      Chen
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      ×
      Goldman
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      BS;
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WPI; 2004-061375/06

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM39674 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 611 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                       26-DEC-2000;
                                                                                                                                            WO200153312-A
                                                                                                                                                                                                                                                                                                                                             Human polypeptide
                                                                                                                                                                                                                   leukaemia.
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                                                                       2000WO-US034263.
 99US-00471275.
2000US-00488725.
2000US-00552317.
                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 828 AA
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Pred. No. 17;
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beptide from a
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RESULT 9
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XX AAB9
XX AAB9
XX Huma
XX Huma
XX BF10
XX EP10
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Matches
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the untiliserious fe has activities with the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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Wang
Zhou
                                                                                                                  29-JUL-1999;
                                                                                                                                                                                28-JUL-2000;
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N-PSDB; AAI58830.
                                                                                                                                                                                                                                           07-FBB-2001.
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB92977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the printed specification
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Wang Z,
Goodrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system
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; 2000US-00620312.
2000US-00653450.
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; 2000US-00727344.
99JP-00300253.
2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                  99JP-00248036
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1 R, Drma
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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66.7%;
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Pred. No. 24
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Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                           03-OCT-2001;
14-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T,
                                                                                                                   02-OCT-2002; 2002WO-US031287.
                                                                                                                                                                                 10-APR-2003
                                                                                                                                                                                                                                         WO2003029421-A2
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NM_015046 protein #SEQ ID 96.
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(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8;
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                                                                                                                                                                                                                                                                                                                                                               discovery;
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Sugiyama T, Wakamats
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                               2001US-0326526P.
2002US-00144194.
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; clinical medicine; forensic medicine.
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Pred. No. 24;
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A, Nagai K,
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C, Otsuki
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e a primer set comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>;</u>
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                Clark H,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions relating to breast cancer, and may be used in gene therapy or antisense therapy. They can also be used in research, drug discovery, clinical medicine and forensic medicine. Sequences given in records ABR58324-ABR58345 represent known polypeptides encoded by polynucleotides that are differentially-regulated in breast cancer. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentially-regulated in breast cancer. The methods and compositi of the present invention are useful for detecting, diagnosing, stagimonitoring, prognosticating, preventing and/or treating diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
          New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mecrenal disease, or demyelinating diseases of the central or periph
                                                                                                                                                                                                                                                                                                                                  PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                      WPI; 2004-419628/39.
N-PSDB; ADP23317.
                                                                                                                                                                                       01-NOV-2002; 2002US-0423394P
                                                                                                                                                                                                                                                21-MAY-2004
                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                          PRO polypeptide SEQ ID NO:412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381623/36
                                                                                                                                                                                                                   30-OCT-2003; 2003WO-US034312
                                                                                                                                                                                                                                                                           WO2004041170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP23318 standard; protein; 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RILXCA-SNXAVDXL
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                                                                                                                                                            GENENTECH INC
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                                                                                                                               Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 96; 127pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                               Van Lookeren M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated polynucleotides which are
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1; Mismatche
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                                                                                                                                  Wood
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1.

or peripheral immune-mediated

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AAM80279
ID AAM80
XX AAM80
XX O6-NO
XX O6-NO
XX Human
XX Human
XX Human
XX Homo
XX O9-AU
XX O9-AU
XX O1-FE
PR 20--U
PR 19--U
PR 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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03-PEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft-versus-host disease.
of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide encoded by it. A protein of the invention nas
antiinflammatory, antiarthritic, antitheumatic, immunosup
osteopathic, antidiabetic, dermatological, articlity, a
                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy at most factor; haematopoiesis; tissue growth factor; humunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein SEQ ID NO 3925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 828 AA;
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                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US004098
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   2000US-00560875.
2000US-00598075.
2000US-00620325.
2000US-00654936.
2000US-00653351.
2000US-00693351.
2000US-00728422.
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                                                                                                                                                                                                                                    2000US-00496914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 829
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66.7%;
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Pred. No. 24;
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RESULT 13
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Best Local S
Matches 10
23-DEC-1999;
21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
Ma Y,
                                                                                                                                                                                                                                 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                            26-JUL-2001
                                                                                                                                                                     WO200153312-A1
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                        Human; nootropic;
                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 6391.
                                                                                                                                                                                                                                                                                                                                             22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 469-470; 6221pp; English
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                                                                                                                  26-DEC-2000;
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                                                                                                                                                                                                                          eukaemia.
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Y, Zhao QA, w
AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
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2000US-00488725
2000US-00552317
2000US-00598042
2000US-00620312
2000US-00623450
2000US-00662191
2000US-00662191
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                                                                                                                    2000WO-US034263
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                                                                                          99US-00471275
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Wejhrman
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therapy.
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Pred. No. 24;
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J, Zhang Goodrich R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
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RESULT 14
AAM79295
IID AAM79
XX AAM79
XX AAM79
XX O6-NC
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX O5-FE
XX O3-FE
PR 20-JU
PR 119-JU
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Best Local 9
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                           03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, archivities and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
Wang
                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory.
                                                                                                                          05-FEB-2001; 2001WO-US004098
                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                       WO200157190-A2
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                               Human protein SEQ ID NO 1957.
                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                            AAM79295;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAM79295 standard; protein; 966 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442253/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 RVLVCAPSNAAVDEL 168
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Wang Z, Weh
Goodrich R,
                                                                                                                                                                                                                                                  system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RILXCA-SNXAVDXL 14
           ; 2000US-00496914.
; 2000US-00560875.
2000US-00598075.
; 2000US-00620325.
; 2000US-00654936.
; 2000US-0063561.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
 2000US-00693325
                                                                                                                                                                                                                                                disorder; arthritis;
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.1%;
66.7%;
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Drmanac RT;
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ĸu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.5;
Pred. No. 24;
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Yang Y,
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Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK51435) and the encoded polypeptides (AAM7823-AAM80302) that exhibit activity elating to cycokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and crivity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                               Yeast; nonsense-mediated mRNA decay pathway; NMD2; UPF3; UPF1; upf19; upf39; gene therapy; beta-thalassmaemia; cancer; polycystic kidney disease; Duchenne muscular dystrophy; Fanconi anaemia; haemophilia; hypercholesterolaemia; neurofibromatosis; Tay-Sachs disease, glycogen storage disease; cystic fibrosis; adenomatous polyposis coli; cowden disease; Maple syrup urine disease; Wilson disease; Niemann-Pick disease; Turcot syndrome; McArdle disease;
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                                       20-JAN-1995;
21-OCT-1997;
                                                                                                                                                                       Saccharomyces
                                                                                                                                                                                                    ornithine transcarbamylase deficiency.
                                                                                                                                                                                                                                                                                                                                   Yeast Upflp.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAY98057 standard; protein; 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 4368-4370; 6221pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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N-PSDB; AAK52428.
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                                                                                                               06-JUN-2000
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Y, Zhao QA,
AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
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Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966 AA;
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                                                                                                                                                                         cerevisiae.
                                       95US-00375300.
97US-00955472.
                                                                                    98US-00177431.
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Wejhrman
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Wang D, Wang
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Pred. No. 28;
1; Mismatches
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J J, Zhang
Goodrich R
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J, Ren F,
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(UYMA-) UNIV

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Job time : 72.8045 secs
                                                                                                                                                                                                                                                                                                                                                                       The nonsense-mediated mRNA decay pathway has an important role in the clear degradation of mRNA transcripts that contain a stop codon. The products of the UPP1 and UPF3 genes (proteins Upf1p and Upf3p, respectively) are essential components of this pathway. Mutations in these genes or chibition of Upf1p or Upf3p function would lead to stabilisation of mRNA containing premature stop codons. The present sequence is the UPP1 crom Saccharomyces cerevislae. The carboxy terminal of the NMD2 gene protein, Nmd2p, has been found to bind to Upf1p, leading to the NMD2 gene protein, Nmd2p, has been found to bind to Upf1p, leading to the MMD2 gene protein, seediated mRNA decay pathway. Inhibition of this gathway is a useful means of treating disorders caused by the cromatous of nonsense mutations, e.g. breast cancer, polycystic kidney consense, Niemann-pick disease, adenomatous polyposis coli, cystic consenses, Niemann-pick disease, meurofibromatosis, ornithine transcarbamylase deficiency, retinoblastoma, consenses, McArdle disease, colorectal cancer, Tay-Sachs consenses, McArdle disease, colorectal cancer, Tay-Sachs consenses, McArdle disease, colorectal cancer, Tay-Sachs colorenses, Mayerophy, adrenocortical carcinoma, Li-Fraumeni syndrome, Maple syrup urine disease, Turcot syndrome or beta-thalassaemia
                                                                                                                                                                                                            Query Match 71.1%;
Best Local Similarity 73.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testing for compounds able to modulate the nonsense mediated mRNA decay pathway for increasing endogenous protein production by incubating a candidate compound with a cell having a gene with a nonsense mutation and a gene without mutation.
                                                                                                                                                                                                                                                                                                                             Sequence 971 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 57pp; English.
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N-PSDB; AAA39454.
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                                                                                                       He P;
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Result
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Maximum DB
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seq length: 2000000000
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57
1 RILXCASNXAVDXL
                                                                                                                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Listing first 45 summaries
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                    US-09-359-268A-2

US-09-359-268A-29

US-08-724-354D-22

US-09-270-984A-22

US-09-270-984A-22

US-09-270-984A-2

US-09-359-268A-18135

US-09-359-268A-13

US-09-359-268A-26

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US-09-270-984A-4

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US-09-28-796A-19108

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29, Appl
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126, Appl
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15238, A
10394, A
7198, Ap
45608, A
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483, App
20535, A
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4, Appli
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10116, A
16855, A
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31 54.4 294 4 US-09-408-020-12 31 54.4 295 4 US-09-252-991A-26676 31 54.4 323 4 US-09-252-991A-26676 31 54.4 345 4 US-09-252-991A-28728 31 54.4 345 4 US-09-252-991A-28728 31 54.4 362 2 US-08-66762-81. 31 54.4 362 2 US-08-86-762-83. 31 54.4 965 4 US-09-58-092-663 31 54.4 965 4 US-09-58-092-663 31 54.4 2237 1 US-08-455-543A-48 31 54.4 2237 2 US-08-223-305C-48 31 54.4 2237 3 US-08-223-318-2 31 54.4 2237 3 US-08-223-305C-47 31 54.4 2337 3 US-08-453-007-2 31 54.4 2339 1 US-08-453-305C-47 31 54.4 2339 2 US-08-228-163-6	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	
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4 US-09-408-020-12 4 US-09-252-991A-26676 4 US-09-252-991A-20118 US-09-248-796A-20118 US-09-248-796A-20118 2 US-08-846-762-83. 4 US-08-846-762-83. 4 US-08-846-762-83. 4 US-08-846-762-83. 4 US-08-458-092-603 4 US-08-258-092-603 4 US-08-258-092-638 2 US-08-258-092-638 3 US-08-278-305C-48	2339	2339	2339	2337	2337	2237	2237	2237	965	510	362	362	358	345	323	295	294	
US-09-408-020-12 US-09-252-991A-26676 US-09-252-991A-20118 US-09-248-799A-20118 US-09-252-991A-28728 US-09-252-991A-28728 US-08-46-762-13 US-08-46-762-14 US-08-46-762-83 US-09-538-092-650 US-08-455-543A-48 US-08-223-305C-48 US-08-253-305C-47 US-09-452-007-2 US-09-452-305C-47 US-08-233-305C-47	w	ນ	<u>, , , , , , , , , , , , , , , , , , , </u>	w	w	w	ຸນ	۱.,	4	4	ຎ	N	4.	4	a.	da	4.	
	US-09-268-163-6	US-08-223-305C-47	-08	-09	30-	-268-163-	US-08-223-305C-48	US-08-455-543A-48	US-09-538-092-650	US-09-538-092-603	US-08-846-762-83.		US-09-252-991A-28728	US-09-248-796A-20118	US-09-902-540-10675	US-09-252-991A-26676	US-09-408-020-12	
	6, Appli	47, App.	47, App	2, Appli	2, Appl:	8, Appl:	48, App		650, App	•	-		28728, 1	20118, 7	10675, 7	26676, 7	12, App1	

ALIGNMENTS

RESULT 1 US-09-359-268A-2

US/09359268A

GENERAL INFORMATION: Sequence 2, Application Patent No. 6630294

APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: THE FIDELI
TITLE OF INVENTION: THEREOF

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A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES

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FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 32
SOPTWARE: PATENTLE PATENTS OF SEQ ID NO 2
LENGTH: 14
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
TITLE OF INVENTION: A SUBFAMILY OF RNA HELIC
TITLE OF INVENTION: THE FIDELITY OF TRANSLAT
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
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                                                                                                                                                                                                                                                              RESULT 2
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Best Local S
Matches 14
                                                                                                                                                                                 Sequence 29, Application US/09359268A Patent No. 6630294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                      RILXCASNXAVDXL 14
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100.0%;
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Pred. No.
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                                                                                              RNA HELICASES WHICH ARE MODULATORS OF TRANSLATION TERMINATION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid
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PRIOR FILING DATE:

1998-07-22

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RESULT 4
US-09-270-984A-22
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US-08-724-354D-22
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Sequence 22, Application US/09270984A Patent No. 6048965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08724354D Patent No. 5994119
                                                                                                                                                            Matches
                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 38
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/016,48
FILLING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lista A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 971 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/724,354D FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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STREET:
TTY: La Jos
CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson, P.C. STREET: 4225 Excutive Square, Suite 1400
                                                                                               454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 RILVCAPSNVAVDHL 45
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Similarity 73.3%;
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                                                                                             RILVCAPSNVAVDHL 468
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                                                                                                                                                                                                                                                                                  971 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
SYSTEM: Windows95
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jolla
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Pred. No. 2
                                                                                                                                                                         Score 40.5; DB 2; Length 971; Pred. No. 6.7;
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US-09-177-431-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Applic Patent No. 6071700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHAPACTERIA.
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: He, Fe
APPLICANT: Jacobs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: Fish & Richardson P.C.
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 4225 Excutive Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
                                                                                                                                                                           STATE: MA
COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                         CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 92037
                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 RILVCAPSNVAVDHL 468
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                                                                                                                                                                                                                                                                                                                                                                                Allan S.
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Pred. No. 6.7;
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Suite 1400
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APPLICATION NUMBER:

08/955,472

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US-09-248-796A-18135
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: saccharomyces cerevisiae US-09-359-268A-13
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US-09-359-268A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: P.
SEQ ID NO 13
LENGTH: 13
TYPE: PRT
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                 Sequence 18135, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09359268A Patent No. 6630294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USBS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
                CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12
                                                                    APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/093,685 PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                      FILE REFERENCE: 107196.132
PRIOR APPLICATION NUMBER: US 60/074,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
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Local Similarity 73.38;
see 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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)GY: linear
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76.9%;
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0; Mismatches
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; Sequence 1100, Application
; Patent No. 6793314
; GENERAL INFORMATION;
APPLICANT: Giot, Loic
; APPLICANT: Mansfield,
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US-09-538-092-1100
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                                  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using PILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOPTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1100

LENGTH: 993
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PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 26
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dinman, Jonathan TITLE OF INVENTION: A SUBPANTITIE OF INVENTION: THE FIDE TITLE OF INVENTION: THEREOF FILE REFERENCE: 601-1-85N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 66.7%;
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Pred. No. 2
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Pred. No. 4.
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RESULT 11
US-09-270-984A-4
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US-08-724-354D-4
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Best Local Similarity 60.0
Conservative
Sequence 4, Application US/09270984A Fatent No. 6048965
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REC
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                     Query Match
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PILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/016,482
PILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION UNMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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SOFTWARE: FastSEC
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4225 Excutive Square, Suite 1400
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   MAMMALIAN REGULATOR OF
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1; Mismatches
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Pred. No. 74;
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GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                              FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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LENGTH: 1043 amino aci
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: rish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
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NUMBER OF SEQUENCES:
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
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les 9; Conserv
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STREET: 4225 Excutive Square, Suite 1400
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONSENSE-MEDIATED RNA DECAY: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.5%; Score 34.5; DB 3; 64.3%; Pred. No. 1.2e+02;
                                   60/016,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/270,984A
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US-09-270-984A-2
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Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09270984A Patent No. 6048965
                                                            Matches
                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Haile, Liea A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                             TELEPAX: 619-678-5099
NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                   TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1118 amino acti
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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517 VLVCAPSNIAVDQL 530
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                           ILXCA-SNXAVDXL 14
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                                                                                                                                                                                  1118 amino acids
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                                                            Conservative
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SYSTEM: Windows95
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WAMMALIAN REGULATOR OF NONSENSE-MEDIATED RNA DECAY
                                                                         60.5%;
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                                                                         Score 34.5;
Pred. No. 1.
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Pred. No. 1
                                                            Mismatches
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US-09-252-991A-16855
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US-09-949-016-10116
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 16855
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                          Matches
                                                                                                                                                                                                                                                                                FILE REPRENCE: 107196.136
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16855, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.5%;
Local Similarity 64.3%;
nes 9; Conservative
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168 ŘÍAYČÁŠKAGLĎNÍ 181
                                   1 RILXCASNXAVDXL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ILXCA-SNXAVDXL 14
                                                                      Similarity 7; Conserv
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                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                            ON: ABRUGINOSA FOR DIAGNOSTICS 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                 Rubenfield et al.

NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                         59.6%;
                                                                                         Score 34; DB
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5; DB 4;
Pred. No. 1.4e+02;
                                                                        Mismatches
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                                                                                                           4
                                                                                                         Length 259;
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OF DETECTION AND USES THEREOF
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Search completed: April 18, 2005, 08:18:32 Job time : 18.4745 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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Gapop 10.0 , Gapext 0.5
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpaa/US0
/cgn2_6/ptodata/1/pubpaa/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgn2
m2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
m2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
m2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
m2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
m2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
m2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
m2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Regult No.
33333334444 666667300000 66666730000000000000000000	Score
64.0 64.0 64.0	Query Match Length DB
380 611 828 1975 2677 713 139 472 626 637	ength I
11566611566	
US-10-652-334-29 US-10-369-493-10288 US-10-144-194A-96 US-10-437-963-140079 US-10-144-194A-22 US-10-369-493-22762 US-10-652-334-13 US-10-652-334-13 US-10-652-334-26 US-10-652-334-26 US-10-652-334-26 US-10-452-34-25-114-37717	ID
Sequence 29, Appl Sequence 10288, A Sequence 10288, A Sequence 26, Appl Sequence 2762, A Sequence 2762, A Sequence 3, Appl Sequence 36594, A Sequence 36594, A Sequence 26, Appl Sequence 23501, Sequence 37717, A	Description

ALIGNMENTS

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US-10-652-334-2
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                                                                             Query Match
Best Local S
Matches 14
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SEQ ID NO 2
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10652334 Publication No. US20040115787A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPAMILY OF RNA HELICASES
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 601-1-85N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Peltz, Stuart
                                                                                                                                                                                   OTHER INFORMATION: Xaa = any amino acid
                                      1 RILXCASNXAVDXL 14
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Czaplinski, Kevin
                                                                               Conservative
                                                                           89.5%; Score 51; DB 16; Length 14; 100.0%; Pred. No. 0.0027; 1ve 0; Mismatches 0; Indels
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US-10-144-194A-96
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                                                                       RESULT 4
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; ORGANISM: saccharomyces cerevisiae
US-10-652-334-29
Sequence 96, Application US/101 Publication No. US20030215809A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/10652334 Publication No. US20040115787A1
                                                                                                                                                                                                                                                                                                                      ORGANISM: Cytophaga hutchinsonii
3-10-369-493-10288
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 10288
LENGTH: 611
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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                                                                                                                                                                                                                         / Match 71.1%; Score 40.5; I
Local Similarity 66.7%; Pred. No. 15;
1es 10; Conservative 1; Mismatches
                                                                                                                                 215 RVLVCASSNAAVDVL 229
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                         Application US/10144194A
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73.3%;
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                                                                                                                                                                                                                   RESULT 6
US-10-144-194A-22
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                                                                                                         Sequence 22, Application US/10144194A
Publication No. US20030215809A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 2677
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 96
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Best Local Similarity
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SEQ ID NO 140079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                 1170 RVLVCAQSNAAVDEL 1184
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Pred. No. 2:
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Pred. No. 5
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US-10-369-493-22762
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Best Local Similarity 66.7
Matches 10; Conservative
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Publication No. US20030233675A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
ERIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                             APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS
TITLE OF INVENTION: THEREOF PILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/9/359,268A
PRIOR PILING DATE: 1999-07-22
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PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
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TYPE: PRT
ORGANISM: Schizobaccharomyces pombe
FEATURE:
HAME/KEY: unsure
LOCATION: (1)...(712)
OTHER INFORMATION: unsure at all Xas locations
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66.7%;
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Pred. No. 68;
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APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPANILY OF RNA HELICASES WHICH ARE MODUL
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-65N
CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT APPLICATION NUMBER: US/09/359,268A
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR APPLICATION NUMBER: 05/093,685
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR PILLING DATE: 1998-07-22
PRIOR FILLING DATE: 1998-07-22
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TYPE: PRT
; ORGANIEM: Baccharomyces cerevisiae
US-10-652-334-13
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US-10-652-334-26
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 36594
LENGTH: 139
                                   NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 472
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/10652334 Publication No. US20040115787A1
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Best Local
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Best Local Similarity
ORGANISM: saccharomyces cerevisiae -10-652-334-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 KILACAASNIAVDNI 133
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76:9%;
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Pred. No. 21;
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Pred. No. 1.
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US-10-424-599-233501
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US-10-437-963-166322
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US-10-437-963-166322
                                                                                                                                CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233501
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SEQ ID NO 166322
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APPLICANT:
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Publication No. US20040031072A1
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                                                                                                                                                                                                 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (5321) B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                       LENGTH: 637
TYPE: PRT
ORGANISM: Glycine max
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TYPE: PRT
ORGANISM: Oryza sativa
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LOCATION: (1).. (626)
OTHER INFORMATION: unsure at all Xaa locations
                 NAME/KEY: unsure
LOCATION: (1)..(637)
OTHER INFORMATION: unsure
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9; Conserva
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                                                                                                                                                                                                                                                   Cao Yongwei
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Barbazuk, Brad
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                   all Xaa locations
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Pred. No. 97;
2; Mismatches 3;
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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 Best Local Similarity
                   Query Match
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                                                                                                                                    LENGTH:
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bes 9; Conserv
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9; Conserva
64.0%;
60.0%;
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37717
LENGTH: Can
                                                         ; OTHER INFORMATION: Clone ID: LIB3175-019-D10_FLI.pep US-10-425-114-37557
                                                                                                                                                            ; APPLICANT: Tabaska, Jack B; APPLICANT: Cao, Yongwei; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(5313)B; CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 37557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3170-056-H12_FLI.peg-
US-10-425-114-37717
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37557, Application US/10425114 Publication No. US20040034888A1
                                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana columbia
FEATURE:
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Kovalic, David K.
Screen, Steven E
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Pred. No. 9
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Pred. No. 9
Score 36.5;
Pred. No. 99;
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                   DB 15;
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                     Length 642;
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US-10-59-493-1830

(Sequence 1830, Application US/10369493

(Publication No. US20030233675A1

(GENERAL INFORMATION:

(APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: WINTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1830

CRGANISM: Saccharomyces cerevisiae

US-10-369-493-1830
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Search completed: April 18, 2005, 09:04:05 Job time: 49.6642 secs
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US-10-369-493-1830
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Maximum Match 100%
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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38.5
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length: 2000000000
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                T41580
B87153
E70896
S71628
T30608
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T39072
B82544
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      hypothetical probable acyl
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probable phoH2 pro
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probable dna-bindi
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protein T27A10.2 [
                                               hypothetical prote
probable short-cha
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related to SEN1 pr
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probable helicase
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                                                                                                                                                                                                                                  prematurely termin
                                                                                                                                                 protein - yea
      acyltrans
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ALIGNMENTS

prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9583.05c; protein YMR080c; UPP1 protein
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S23408; A44388; \overline{S}54455
C;Accession: S23408; A44388; \overline{S}54455
C;Altamura, N.; Groudinsky, O.; Dujardin, G.; Slonimski, P.P.
J. Mol. Biol. 224, 575-587, 1992
A;Reference number: S23408; MUID:9235815; PMID:1314899
A;Accession: S23408; MUID:92335815; PMID:1314899

A; Molecule type: DNA A; Residues: 1-971 < ALT>

A;Molecule type: DNA A;Residues: 1-971 <GEN> A;Cross references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080c A;Experimental source: strain AB972 C;Genetics: A;Cross-references: GB:M76659; NID:g173141; PIDN:AAA35197.1; PID:g173142
R;GentLes, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54451
A;Accession: S54455 A;Cross references: UNIDROT:D30771; EMBL:X62394; NID:g4022; PIDN:CAA44266.1; PID:g4023 R;Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R. Mol. Cell. Biol. 12, 2165-2177, 1992 Mol. Cell. Biol. 12, 2165-2177, 1992 A;Title: Gene products that promote mRNA turnover in Saccharomyces cerevisiae. A;Reference number: A44388; MUID:92236591; PMID:1569946 A;Accession: A44388; MUID:92236591; PMID:1569946 RESULT 2 D86303 F17F16.1 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) 밁 Ś A;Map position: 13R C;Keywords: GFP binding; mitochondrion; nucleotide binding; nucleus; P-loop F;430-437/Region: nucleotide-binding motif A (P-loop) F;545-548/Region: GTP-binding NKXD motif A;Cross-references: SGD:S0004685; MIPS:YMR080c A;Gene: SGD:NAM7; UPF1 A; Molecule type: DNA A; Residues: 1-971 < LEB> Matches Query Match Match 71.1%; Score 40.5; Di Local Similarity 73.3%; Pred. No. 3.3; es 11; Conservative 0; Mismatches 454 1 RILXCA-SNXAVDXL 14 RILVCAPSNVAVDHL 468 DB 2; ω •• Length 971; Indels 1; Gaps 1;

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                   Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.;
A;Title: Massive gene decay in the
                                                                                        eam, M.A.; Rutherford, K.M.
                                                                                                             R;Cole, S.T.; Eiglmeier, K.; Parkhill, R.; Davies, R.M.; Devlin, K.; Duthoy,
                                                                                                                                                        PhoH-like protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Bate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87153
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A;Accession: T41580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable dna-binding protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe
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  A;Reference number: A86909;
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A;Experimental source: strain 972h(-)
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A;Molecule type: DNA
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A;Residues: 1-2142 <STO>
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Best Local S
Matches 10
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;Superfamily: probable DNA helicase MJ0104
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66.7%;
er, K.; Simon, 9 in the leprosy MUID:21128732;
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Pred. No. 6.5;
1; Mismatches
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, S.; Simmonds, M
sy bacillus.
2; PMID:11234002
                                                                                                                James, K.D.; Feltwell, T.;
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                                                                                                                Thomson,
Fraser, 1
                                          Skelton,
                                                                                                                N.R.; Wheeler,
A.; Hamlin, N.;
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Holroyd,
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Matches
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A; Experimental :
C; Genetics:
A; Gene: phoH2
A;Cross-references: UNIPROT:Q23901; EMBL:X96869
A;Cross-references: UNIPROT:Q23901; EMBL:X96869
A;Experimental source: strain AX2; substrain 214
R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.
submitted to the EMBL Data Library, March 1996
A;Description: The hybrid histidine kinase Doka is part of the off A;Pescription: The hybrid histidine kinase Doka is part of the off A;Pescription: 578068
A;Accession: 578068
A;Molecule type: DNA
A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; C;Genetics:
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A,Status: preliminary
A;Molecule type: DNA
A,Residues: 1-433 <STO>
A;Cross-references: UNIPROT:Q9X792; GB:AL450380; NID:g13093606; PIDN:CAC30906.1; GSPDB:GN
C;Genetics:
A;Gene: phoH2
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09
                                                                                                                                                                                                                                                                                                                           R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; S
EMBO J. 15, 3880-3889, 1996
A;Title: The hybrid histidine kinase DokA is part of the
A;Reference number: S71628; MUID:96324396; PMID:8670893
                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997
C;Accession: S71628; S78068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: E70896
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Nature 393, 537-544, 1998
                                                                                                                                                                                                                                              A; Residues: 1-1670 <SCH>
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A;Experimental source: strain H37Rv
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58.3%;
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Pred. No.
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A; Cross-references: UNIPROT: O81047; EMBL: ACO05313; NID: g3548797; PID: g3548803
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; A; Accession: D84446
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C;Function:
C;Function: modulates cell response to changes in osmolarity; involved
A;Description: modulates cell response to changes in osmolarity; involved
C;Keywords: phosphoprotein; signal transduction
C;Keywords: phosphoprotein; signal transduction
F;1520-1629/Domain: response regulator homology <RRH2>
F;1568/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable helicase At2903270 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T18E12.6 C;Species: Arabidopsis thaliana drouse-ear cress) C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02699; D84446
A;Molecule type: DNA
A;Residues: 1-635 <STO>
A;Cross-references: GB:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z14702
A;Accession: T02699
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T02699; D84446
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Pasubmitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II E
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Science 273, 813-816, 1996
A;Title: Genome sequence of
A;Reference number: Z20876;
A;Accession: T30608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 05-Nov-1999 #sequence_revision C;Accession: T30608
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                                                                                                A;Status: preliminary
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A; Residues: 1-1173 <SEN>
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A; Residues: 1-635 < ROU>
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                         Cross-references: GB:AE002093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.9%;
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Pred. No. 20;
1; Mismatches
                         NID:g4335770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.P.; Fujii, C.Y.; Mason, T.M.; Shen,
                         PIDN:AAD17447.1; GSPDB:GN00139
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1218 KLLVCAPSNAAVDEL

1232

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A;ACtessam, preliminary
A;Status; preliminary
A;Molecule type: DNA
A;Residues: 1-1825 <SCH>
A;Residues: 1-1825 <SCH>
A;Cross-references: UNIPROT:09HF15; EMBL:AL442164; GSPDB:GN00116; NCSP:B2J23.170
A;Cross-references: UNIPROT:09HF15; EMBL:AL442164; GSPDB:GN00116; NCSP:B2J23.170
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R;Shieh, S.Y.; Stellrecht, C.M.; Tsai, M.J.
J. Biol. Chem. 270, 21503-21508, 1995
J. Biol. Chem. 270 characterization of the rat insulin enhancer-binding complex 3b2. Clo. A;Reference number: Z24545; MUID:95394901; PMID:7665561
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A;Map position: 2
C;Superfamily: probable DNA helicase MJ0104
S
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R; Schulte, U.; Aign, V.; Hoheisel,
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A;Molecule type: mRNA
A;Residues: 1-989 <SHI>
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A;Accession: T52521
                                                                                                                                                                                                                                                                                                     submitted to the Protein
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C;Date: 20-Oct-2000 #sequence
                                                                                                                                                                                                                                                                                                                                                                                               related to SEN1 protein [imported] - N; Alternate names: protein B2J23.170
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                                                                                                                               NCSP: B2J23.170
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 1 RILXCA-SNXAVDXL 14
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66.7%;
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                                                      Score 36.5;
Pred. No. 3
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Pred. No. 19
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J.;
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Pred. No. 2
                                       Mismatches
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C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
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C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenecl
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   avanagh, T.
Nature 391,
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A;Residues: 'MHS',130,'FCEREVQ',131-2231 <DEM>
A;Cross_references: GB:M74589; NID:g172573; PIDN:AAB63976.1; PID:g172574
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Accession: E71420
3;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel P.; Wedler, E.; Wambutt, R.; Weitzenegger, M.; Schaeffer, M.; Funk, B. avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, B. avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, B. avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Pons, A.; Puigdomenech
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LiResidues: 1-231 < FAV>
LiCross-references: UNIFOT:Q00416; EMBL:U20939; NID:g664871; PID:g664872; MIPS:YIR430w; Cross-references: University Capacity Capacit
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;Accession: S53416; A44387; S41985
                                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPROT:023408; GB:Z97339; NID:g2244901;
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Pred. No. 44
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Pred. No. 21;
3; Mismatches
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                                                                                   RESULT 15
    tRNA-splicing endonuclease positive effector - C;Species: Schizosaccharomyces pombe
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Ig mu chain switch region binding protein 2 - human (Alternate names: DNA-binding protein S-mu-bp-2; glial factor 1; transcription C;Species: Homo sapiens (man) C;Date: 02-Jun-1995 #semmence reministration of the contract 
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R;Kerr, D.; Khalili, K.
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Mizuta, T.R.; Fukita, Y.; Miyoshi, T.; Shimizu, A.; Honjo, Nucleic Acids Res. 21, 1761-1766, 1993
A;Title: Isolation of cDNA encoding a binding protein specif. A;Reference number: 835633; MUID:93261806; PMID:8493094
A;Accession: S35633
A;Status: preliminary; nucleic acid sequence not shown
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A;Title: The human Smubp-2, a DNA-binding protein specific to the single-stranded A;Reference number: A47500; MUID:93352537; PMID:8349627
                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-993 <MIZ>
A;Cross-references: UNIPROT:P40694; GB:Ll0075; NID:g293805; PIDN:AAA40143.1; PID:g293806
C;Keywords: DNA binding
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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A;Map position: 11q13.2-11q13.4
C;Keywords: immunoglobulin; single-stranded DNA binding
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A;Title: A recombinant cDNA derived from human brain encodes
A;Reference number: A40804; MUID:91340730; PMID:1714899
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A;Residues: 'GRV',495-862,'K',864-865,'T' <KER>
A;Cross-references: GB.M64979; NID:g183249; PIDN:AAA58611.1; PID:g183250
A;Experimental source: brain stem
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A; Residues: 1-993 < FUK>
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C;Bate: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C;Accession: A4750; A40804
R;Fukita, Y:; Mizuta, T.R.; Shirozu, M.; Ozawa, K.; Shimizu, A.; Honjo, T.
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Pred. No. 3
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Pred. No. 35
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C_Dete: 03_Dec_1999 Becquence_revision 03_Dec_1999 #text_change 09_JU1-2004
C_Accession: TQ065
R_LVMe, M.; Rafandream, M.A.; Berrell, B.G.; Lelaurre, V.; Gallbert, F.
submitted to the BME Date Lichtrery, December 1998
A_Rectance number: Z21903
A_RCCESSION: TY0055
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Mis Page Blonk (Usbio)

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 2 Q6ZQ81 ID Q6ZQ AC Q6ZQ DT 05-J DT 05-J DT 05-J DT MKIA GN Name OC Euka 맑 á Query Match Best Local S Matches 10 Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003). EMML; BX294136; CAD72321.1; -. R GO; GO:0005524; F:ATP binding; IEA. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0003166; F:nuclectide binding; IEA. R GO; GO:0000166; F:nuclectide binding; IEA. R GO; GO:0001593; AAA ATPABASE. R InterPro; IPR001593; AAA ATPABAST; SM00382; AAA; 1. R SMART; SM00382; AAA; 1. R SMART; SM00487; DEXDC; 1. W ATP-binding; Complete proteome; DNA-binding. SEQUENCE 763 AA; 84494 MW; A9DA57C245BOBCCE CRC64; Q7UWP1 Q7UWP1; Q7UWP1; Q7UWP1; Q1-OCT-2003 (TrEMBLrel. 25, La Q1-OCT-2003 (TrEMBLrel. 25, La Q1-MAR-2004 (TrEMBLrel. 26, La DNA-binding protein SMUBP-2. QrderedLocusNames=BB1895, Rhodopirellula baltica. Q6ZQ81 PRELIMINARY; Q6ZQ81; Q5ZQ81; O5-JUL-2004 (TrEMBLrel. 27, Li 05-JUL-2004 (TrEMBLrel. 27, Li 05-JUL-2004 (TrEMBLrel. 27, Li MKIAA0625 protein (Fragment). MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula "Toron Note" and the sequence of the servine planctomycete Pirellula "Toron Note" and "Tor SEQUENCE FROM N.A. Bacteria; Planctomycetes; Pla Planctomycetaceae; Pirellula. NCBI_TaxID=117; 356 1 RILXC-ASNXAVDXL 14 l Similarity 10; Conserv RVLACAASNTAVDNL 370 72.8%; nilarity 66.7%; Conservative Planctomycetacia; Planctomycetales; Created) Last sequence update) Last annotation update) ŗ Last sequence update) Score 41.5; DB 2; Pred. No. 6.5; Created) PRT; ed. No. 6.5; Mismatches 778 763 ⋛ ⋧ update) Length 763; Indels 1, Gaps ďB ۲

MKIAA0625 protein (Fragment). Name=mKIAA0625; Mus muscullus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Wedwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Van Hollon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Milting M., Walan A., Schmutz J., Myers R.M., Butterfield Y.S.,

Kores S. T. Marra M. A., Schmutz J., Myers R.M., Schein J.E.,

Kores S. T. Marra M. A., Schmutz J., Schmerch A., Schein J.E.,
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Name=AMO60766;
Mus musculus (Mouse).
Merazoa; Chordata;
Merazoa; Rodentia;
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Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
DNA Res. 10:167-180(2003)
Submitted (AUG-2004)
                          STRAIN=C57BL/6; TISSUE=Brain; Director MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                     full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PRREAD REPORT OF THE PRESENTATION OF THE PRESE

RESULT 5
Q6AZD7
ID Q6AZ
AC Q6AZ

Q6AZD7 Q6AZD7;

PRELIMINARY;

PRT;

917

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RESULT 4
Q80V90
ID Q80V
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                                                                                                                                                                                                                                                                                                                                                                     RX MEDLINE-2238657; Pubmede12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Duetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Ugdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
ROBER S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
N. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
N. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
N. A. Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
                                                                     Matches
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q80V90;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q80V90
                                                                                                                                                              MGD; MG
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TREMBLIEL: 24,
01-JUN-2003 (TREMBLIEL: 24,
01-MAR-2004 (TREMBLIEL: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC058109; AAH58109.1; -.
EMBL; BC079604; AAH79604.1; -.
SEQUENCE 821 AA; 92120 MW;
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                      STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                          and mouse
                                                                                                                                                                                                                                                                                                                                         "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                            Jones S.
                                                                                      Local
                                                                                                                                                                         , BC046382; AAH46382.1;
MGI:2139292; AW060766.
234
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                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                            J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                     FROM
                                RILXCA-SNXAVDXL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RILXCA-SNXAVDXL
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                                                                                                                                                                                                                                                                                                                        cDNA sequences.
                                                                                                                                                                                                                 (FEB-2003) to the
                                                                                                                                         902 AA;
                                                                                                                                                                                                                                                   TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary tumor. Brca1-/fl;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                           101988 MW;
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66.78;
                                                                                    71.1%;
66.7%;
                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                      tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                   ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲
                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
                                                                                      Score 40.5;
Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.5;
Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                           99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB28DFCA91698287 CRC64;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                           E4356FB7063D9D4F CRC64;
                                                                                                                                                                                                                                                      Brcal-/fl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                902
                                                                                        12;
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                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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••
                                                                                                       Length 902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                             full-length human
                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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PAC OCCUPANTO CONTROL OCCUPANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTISSUE-Peripheral Nervous System;
CTISSUE-Peripheral Nervous Strauber L., Derge J.G.,
CSCHuler G.D.,
CSCHULER, CSCHULER, CSCHULER C.M., Schaler G.D.,
CALLANDER C.F., Dellins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
CALLANDER C.F., Jordan H., MOORE T., Max S.I., Wang J., Hsieh F.,
CALLANDER C.F., Jordan H., MOORE T., Max S.I., Wang J., Hong L.,
CALLANDER C.F., Jordan H., MOORE T.A., Rubin G.M., Hong L.,
CALLANDER C.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CALLANDER C.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CALLANDER C.F., Casavant T.L., Scheete T.E.,
CALLANDER C.F., Casavant T.L., Scheete T.E.,
CALLANDER C.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CALLANDER C.F., Casavant T.L., Scheete T.E.,
CALLANDER C.F., Casavant T.L., Schein J.E.,
CALLANDER C.F., Casavant T.L., Maxavant T.L., Schein J.E.,
CALLANDER C.F., Casavant T.L., Casavant T.L.,
CALLANDER C.F., Casavant T.L., Casavant T.L.,
CALLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6FVZ1
Q6FVZ1;
O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome D complete
ORRNames-CAGLOD043129;
Candida clabrata communication complete
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuvegiise C., Talla E., Goffantaine I., Harden J., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida glabrata CBSI38.
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                               Genolevures;
                                                                                                                                                                                                                                                                         STRAIN=CBS138;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
NON_TER
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"Generation and initial analysis
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Peripheral Nervous System,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
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                                                                                                                                                                                                                                                                                                                                 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RILXCA-SNXAVDXL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.1%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.5; D
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycotina;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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RESULT 7
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Ol-JUL-1993 (Rel. 26, Last sequence update)
O5-JUL-2004 (Rel. 44, Last annotation update)
NAM7 protein ((Nuclear accomodation of mitochondria 7 protein)
Nonsense-mediated mENA decay protein 1) (Up-frameshift suppressor 1).
Nonsense-mediated mENA decay protein 1) (Up-frameshift suppressor 1).
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01-JUL-1993
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                                                                                 STRAIN=S288c / AB972;
MEDLINE=97131268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt
Connor R., Dedman K., Devlin K., Gentles S., Rajandram
Jagels K., Lye G., Moule S., Odhit C., Pearson D., Rajandram
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
The nucleotide sequence of Saccharomyces cerevisiae chromoson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interro, IPR06935; Re
Pfam, PF04851; ResIII;
cwhpT: SM00487; DEXDC;
                                                                                                                                                                                                                                  "Gene products that promote mRNA cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CHARACTERIZATION.
MEDLINE=97051830; PubMed=8896465;
Cui Y., Dinman J.D., Peltz S.W.;
                                                                                                                                                                                                                                                                                                                         Saccharomyces
J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92235815; PubMed=1314899;
Altamura N., Groudinsky O., Dujardin G.,
"NAM7 nuclear gene encodes a novel membes
with a Zn-ligand motif and is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=R23/50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                          Nature
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                 Leeds P.F., Wood J.M.,
                                                                                                                                                                                                                                                                             MEDLINE=92236591; PubMed=1569946;
                                                                                                                                                                                                                                                                                              SEQUENCE
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224:575-587(1992)
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aire M., Lesur I., Ma L., Muller H.,
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Pred. No. 13
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lved in mitochondrial functions
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RESULT
Q9FWR3
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Best Local Similarity
                                                                                           Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P. Toriumi M., Vaysberg M., Yu G. Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FWR3;
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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-!- SUBCELIAULAR LOCATION: Present predominantly in the cytoplasm, is also found in small quantities in the nucleus.
-!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
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PIR; D86303; D86303.
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EMBL; M76659; AAA35197.1; -.
EMBL; Z49259; CAA89226.1; -.
PIR; S23408; S23408.
  SEQUENCE
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SMART; SM00487; DEXDC; 1.
ATP-binding; Helicase; Hydrolase; Mitochondrion;
Nonsense-mediated mRNA decay; Nuclear protein; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; AAA ATPase.
InterPro; IPR001410; DEAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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GO:0005737; C:cytoplasm; IDA.
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                         CO; IPR011545; DEAD/DEAH_N. SM00487; DEXDC; 1.
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q68DW5;
25-OCT-2004
25-OCT-2004
                                                                 Moreira M.C., Klur S., Watanabe M., Nemeth A.H., Le Ber I., Moniz J.C., Tranchant C., Aubourg P., Tazir M., Schols L., Pandolfo M., Schulz J.B., Pouget J., Shizuka-Ikeda Shoji M., Tanaka M., Izatt L., Shaw C.B., M'Zahem A., Dunne E. Bomont P., Benhassine T., Bouslam N., Stevanin G., Brice A., Guimaraes J., Mendonca P., Barbot C., Coutinho P., Sequeiros Jurr A., Warter J.M., Koenig M., "Senataxin, the ortholog of a yeast RNA helicase, is mutant in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Last sequence up
Hypothetical protein DKFZp781B151 (Fragment)
Name=DKFZp781B151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koehrer K., Beyer A., Mewes )
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2004) to the |
EMBL; CR749249; CAH18105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
SEQUENCE
                                                           ocular apraxia 2.
                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
PubMed=14770181;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Senataxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6IMG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6IMG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q68DWS
                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Setx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RILXCA-SNXAVDXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVLVCAPSNAAVDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RILXCA-SNXAVDXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                         36:225-227(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
N.A
                                                                                                                                                                                                                             DOI=10.1038/ng1303;
ur S., Watanabe M., Nemeth A.H.,
                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.1%;
66.7%;
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66.7%;
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8, 28
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27,
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Last annotation update)
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 30;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                          Sequeiros J.,
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                                                                                   mutant in ataxia-
                                                                                                                                                                Dunne E.,
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RESULT 11
SETX HUMAL
ID SETX AC Q723
DT 05-JJ
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, VAR CYS-1152, ASP-1192; GLY-1252 AND ILB-1386, AND VARIANTS AOA2 CYS-TRP-332; LEU-413, SER-1756 AND LEU-2213.

PubMed=14770181; DOI=10.1038/ng1303;

PubMed=14770181; DOI=10.1038/ng1303;

Moreira M.-C., Klur S., Watanabe M., Nemeth A.H., Le Ber I., Moniz J.-C., Tranchant C., Aubourg P., Tazir M., Schoels L., Pouget J., Calvas P., Shizuka-Ikeda M., Sandifo M., Schulz J.B., Pouget J., Calvas P., Shizuka-Ikeda M., Sandifo M., Tanaka M., Izatt L., Shaw C.E., M'Zahem A., Dunne E., Bomont P., Benhassine T., Bouslam N., Stevanin G., Brice A., Guimaraes J., Mendonca P., Barbot C., Coutinho P., Sequeiros J., Bouslan N., Watter J.-M., Koenig M.,
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SETX HUMAN
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05-JUL-2004 (Rel. 44, Created) 
05-JUL-2004 (Rel. 44, Last sequence update) 
05-JUL-2004 (Rel. 44, Last annotation update) 
Probable helicase senataxin (EC 3.6.1.-) (SEN1 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocular apraxia 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Senataxin, the ortholog of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=SETX; Synonyms=KIAA0625,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genet. 36:225-227(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Teratocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT VAL-2587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM 2),
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66.7%;
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he sequence shown here is
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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derived from
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                  Y., Okamoto S.,
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Klausnerg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,
RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Milting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickeon M.C.,
RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T. Proc. Natl. Acad. Sci T.
Chen Y.-Z., Bennett C.L., Huynh H.M., Blair I.P., Puls Dierick I., Abel A., Kennerson M.L., Rabin B.A., Nicholl Auer-Grumbach M., Wagner K., De Jonghe P., Griffin J.W., Pischbeck K.H., Timmerman V., Cornblath D.R., Chance P.I. TDNA/RNA helicase gene mutations in a form of juvenile in TONA/RNA helicase gene mutations in a form of juvenile in Lacal B. Cherosis (ALSA).";

Am. J. Hum. Genet. 74:1128-1135(2004).

-i- FUNCTION: Probable helicase, which may be involved:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satch T., Shirai Y., Takahashi Y., Nakagawa K., Mizushima-Sugano J., Satch T., Kikuchi H., Masuho Y., Yamashita R., Okumura K., Nagase T., Numura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                   VARIANTS ALS4 SER-389 AND HIS-2136, AND TISSUE SPECIFICITY PubMed=15106121; DOI=10.1086/421054;
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[8]
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Kotani H., Nomura N., Ohara O.;
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Togashi T., Oyama M., Hata H., Watanabe M., Komats
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                                                                                                   maturation (By similarity).
SUBCELLULAR LOCATION: Nuclear
ALTERNATIVE PRODUCTS:
                                                 IsoId=Q7Z333-1;
                  IsoId=Q7Z333-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 15-2677 PROM N.A. (ISOFORM 1), AND VARIANTS GLY-1252 AND
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Bahr A., Mewes H.
an M., Wiemann S.;
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Sequence=VSP_010532, VSP_010533; ental confirmation available;
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Note=No

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: Defects in SETX are a cause of amyotrophic lateral sclerosis 4 (ALS4) [MIM.602433]. ALS4 is a rare, childhood- or adolescent-onset, autosomal dominant form of amyotrophic lateral sclerosis that is characterized by slow disease progression, limb weakness, severe muscle wasting, and pyramidal signs associated with degeneration of motor neurons in the brain and spinal cord. Amyotrophic lateral sclerosis denote a heterogeneous group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AOA2) [MIM:606002]. AOA2 is an autosomal recessive adolescent-onset cerebellar ataxia with additional oculomotor apraxia or with associated elevated serum alpha-fetoprotein (AFP), immunoglobulins and creatine kinase levels but no oculomotor apraxia. Most affected individuals have both oculomotor apraxia and elevated AFP levels. The most debilitating feature of the AOA syndrome is the progressive neurodegeneration associated with loss of Purkinje cells and ectopic location of these cells in the molecular layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory muscles.
SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
CAUTION: Ref. 3 (CAD97857) sequence differs from that
a frameshift in position 1626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             severe, progressive neurological disorders associated with degeneration of motor neurons in the cerebral cortex, brain stem, and spinal cord. ALS4 includes a long duration of disease, absence of overt sensory abnormalities, and the sparing of bulbar and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and lung.
DISEASE:
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BX538166; CAD98045.1;
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AK001456; BAA91701.1;
AK0022902; BAB14299.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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AAH32622.1;
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/FTId=VSP_010533.
T_-> I (in ALS4; heterozygous).
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                                              family)
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Algerian family)
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L -> S (in ALS4; heterozygous)
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Lafontaine I., de Montigny J., Marck C., Neuvegilse C., Talla E.,
Goffard N., Frangeul L., Algle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet. H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachburi R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire S., Ozter-Ralogeropoulos O.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Ralogeropoulos O.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Ralogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Witth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
B Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincher P. Schrifer T.
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Q75DS7;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome;
1140 of Kluyveromyces lactis.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases EMBL; CR382122; CAH02214.1; -. InterPro; IPR006935; ResIII.
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Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000504; RNA_rec_mot.
Pf4am; PF04851; ResIII; 1.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SEQUENCE 969 AA; 108943 MW; 208C14F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames=KLLA0B06435g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            десжев
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                                                                                                                                                                                                                                                                            452
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                                 (TrEMBLrel.
                                                  (TrEMBLrel.
                                                                                                                                       PRELIMINARY
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                                                                                                                                                                                                                                                                                                                                                                                                        69.3%;
66.7%;
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66.7%;
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                            Last sequence update)
Last annotation updat
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Pred. No. 36;
1; Mismatches
                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.5;
Pred. No. 2:
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,
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Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.

ORFNames=ABR022C;

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RESULT 14
Q88E60
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                                                                                                                                                                                                                                                      InterPro; IPR007627; Sigma70 r2.
InterPro; IPR007630; Sigma70 r4.
Pfam; PF045452; Sigma70 r2; 1.
Pfam; PF04545; Sigma70 r4; 1.
Complete proteome.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
RNA polymerase signal of factor, ECF subfamily.
Ordered contains at the contains and the contains at the contains a
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ATP-binding.
SEQUENCE 1000 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=22423060; PubMed=12534463;
Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Holmes M.,
Martins dos Santos V.A.P., Pouts D.B., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple B.K., Scanlan D., Tran K.,
Moazez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB016815; AAS50792.2; -.
GO; GO:0000166; F:nuclectide binding;
InterPro; IPR003593; AAA ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=PP4608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2004)
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Voegeli S.E., Dietrich F.S.,
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; PP4608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiewitz C.,
Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=33169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=160488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0016987; F:sigma factor activity; IEA. GO:0003700; F:transcription factor activity; IEA. GO:0006355; F:regulation of transcription, DNA-de GO:0006352; F:transcription initiation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE016791; AAN70181.1;
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                                                                         Similarity 7; Conserv
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191 AA;
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       ILXCASNXAVDXL 14
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                                                                                                                                                                                                                               21313 MW;
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1; Mismatches
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Pred. No. 22;
                                                                                                                   Score 39; DB Pred. No. 5.6;
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                                                                                                                                                                                                                               505CB7619978B999 CRC64;
                                                                                Mismatches
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                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000013515 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=ENSANGG00000011026
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202
                                                                                                                                                                                                                                                                                                                                           AAAB01008960; EAA11070.2;
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                                                          1 RILXCA-SNXAVDXL
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9; Conser
RVLVCASSNTAVDVI 216
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611 AA;
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ilarity 60.0%;
Conservative
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Search completed: April 18, 2005, 08:15:39 Job time : 61.4526 весв

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
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1: geneseqp1980s:*
2: geneseqp21990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                       Query
Match
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Gapop 10.0 , Gapext 0.5
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54
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60.2
59.3
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650
310
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352
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           ADS42927
ADN47941
ABO69101
AAO17597
ABU19323
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ADS43005
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ABM67035
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ADB07940
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ABU34245
ADN19868
                                                                                                                                                                                                                                                                       ADP44105
AAY77806
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                                                                                                      Abw01179 Saccharom
Adp44105 Yeast tra
Aay77806 Motif III
Adn20231 Bacterial
Abp26966 Streptoco
Abu34245 Protein e
Adn19868 Bacterial
Ads44332 Bacterial
Ads44332 Bacterial
Adk68058 Female re
Adn21359 Bacterial
Abb07916 Pseudomon
Adb07940 Alloiococ
Adb07940 Alloiococ
Adb07946 Alloiococ
                                                                                                                                                                                                                                                                                                                          Description
                                 Aspergill
Photorhab
Bacterial
Thermococ
Pseudomon
                                                                                                Bacterial
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28	28	28	28	28	28	28	28	28	28	28.5	29	29	29	29	29	29	29	29	29
51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9		52.8	53.7	53.7	53.7	53.7	53.7	. 53.7	53.7	53.7	53.7
308	305	289	260	200	131	131	75	75	30	869	988	971	971	971	925	413	393	380	380
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ABP27036	ADA35158	ADN18563	ADS28056	ABO75002	ABM37744	AAU41225	ABM57579	AAU61060	AAW36514	ADM25464	AA026745	ADK64706	ABR53412	AAY98057	ADN19434	ADL04843	ADM25562	ADP44131	ABW01205
Abp27036	Ada35158	Adn18563	Ads28056	Abo75002	Abm37744	Aau41225	Abm57579	Aau61060	Aaw36514	Adm25464	Aao26745	Adk64706	Abr53412	Aay98057	Adn1,9434	Ad104843		Adp44131	Abw01205
Streptoco	Acinetoba	Bacterial	Bacterial	Pseudomon	Propionib	Propionib	Propionib	Propionib	Human REN	Hyperther	988-mer r	Disease t	Protein 8	Yeast Upf	Bacterial	M. catarr	Hyperther	Yeast hel	Saccharom

ALIGNMENTS

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RESULT 1
ABW01179
ID ABWC
XX
AC ABWC
XX
/label= Unknown
/note= "Xaa may
Misc-difference 10
                                                   07-OCT-2003.
                                                                                                 Misc-difference
                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae motif III peptide
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                                                                                                                                                                                                                                                                                                                                                    ABW01179. standard; peptide; 17
                     22-JUL-1998;
                                   22-JUL-1999;
                                                                  US6630294-B1
                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                therapy; HCSB; nonsense mutation; yeast.
                                                                                                                                                                                                                                                                                         Modulator of translation termination; MTT1; helicase B; antiviral;
                                                                                                                                                                                                                                                                                                                       15-JAN-2004
      (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
                                                                                                                                                                                                                                                                                                                       (first entry)
                     98US-0093685P.
                                    9908-00359268
                                                                                                                       /label= Unknown
/note= "Xaa may
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                                                                                                       /label= Unknown
/note= "Xaa may
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/note= "Xaa may be
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Aao17597 Abu19323 Adn47941 Abo69101

E gossypi Protein e Yeast Upf

WPI; 2004-449400/42

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RESULT 2
ADP44105
ADP44105
AD ADP4
AC ADP4
AC ADP4
AC Yeas
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Pamilial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mttl.
                                                                                                                                                                                             22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                          Peltz S,
                                                                              (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
(DINM/) DINMAN J D.
                                                                                                                                                                                                                                                                              28-AUG-2003; 2003US-00652334
                                                                                                                                                                                                                                                                                                                                                                                             US2004115787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast translation
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                             Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Czaplinski
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99US-00359268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termination modulation protein motif III.
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100.0%; Pred. No.
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                             Dinman
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0.0046;
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CC the RNA helicase MTI with a composition or agent under conditions
CC specific binding between the MTI and the composition, detecting
CC specific binding of the test composition or agent to the MTI. The
CC determining if the test composition or agent to the MTI. The
CC composition and methods are useful for modulating the fidelity of
CC translation termination or for identifying agents that: affect the
CC functional activity of mRNAs by altering frameshift frequency, permit
CC transcripts, and provide modulators (inhibitors/stimulators) of peptidyl
CC transferase activity during initiation, elongation, termination and mRNA
CC degradation of translation. The agents, which may be antagonists or
CC agonists, are useful in screening, diagnostic and therapeutic purposes,
CC for diseases or conditions resulting from or cause premature translation,
CC such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular
CC Dystrophy, Haemophilia A, Haemophilia B, Von Willebrand Disease,
CC Osteogenesis Imperfecta, Breast cancer, Ovarian Cancer, Wilms Tumour,
CC Hirschlesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis,
CC Retinoblastoma, ATM or Costmann Disease. The present sequence represents
CT the amino acid sequence of the yeast translation termination modulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTTI with the test composition or agent, and determining if the test composition or agent inhibits the MTTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 35; SEQ ID NO 3; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to modulates the efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to a method of identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of translation termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising
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            S
                             Matches
                                          Query Match
                                    Local
                             17;
             1 VVIDEXXQAXXXXXIPI 17
                                    Similarity
                            Conservative
                                    74.1%;
100.0%;
                                    Score 40; Pred. No.
                            0
                              Mismatches
                                    DB 8; I
                              <u>..</u>
                                           Length 17;
                              Indels
                             0
                             Gaps
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Sequence 17

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RESULT 3
AAY77806
ID AAY7
XX AAY7
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Motif III comprised in a gene modulating translation termination

Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.

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Misc-difference
             Location/Qualifiers
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Unidentified.

WO200005586-A2 /note= "reisdues indicated Xaa are unspecified"

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22-JUL-1998;
                      22-JUL-1999;
98US-00120435
                      99WO-US016802
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(UYNB-) UNIV NEW JERSEY

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RESULT 4
ADN2031
ID ADN2
XX ADN2
XX ADN2
XX Bact
XX Pect
XX Rect
XX Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC transferase activity, especially diseases resulting from a nonsense or CC frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker CC Muscular Dystrophy etc. It can be used to identify disease conditions CC involving a defect in the complex, by transfecting cells with encoding concleic acid and determining the proportion of defective complex before and after transferase activity during translation, inhibiting the complex level in the ransferase activity during translation, inhibiting the complex expression and so modulate encoding translation. Vectors comprising polynucleotides encoding translation cells to can be constructed and introduced into cells to contranscripts in a cell. Agents binding to the complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation of aberrant complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation termination of mRNA and/or during translation termination of mRNA at a nonsense codon and/or promote degradation of aberrant compositions modulate the efficiency of translation termination of compositions modulate the efficiency of translation termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                               Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                             Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN20231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN20231 standard; protein; 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulate peptidyl transferase activity during translation in a cell. I can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the gene encoding Helicase B (HCSB) renamed mTT1, for Modulator of Translation Termination) and the conserved proteins known to interaccarry out translation termination in eukaryotto cells, peptidyleukaryotic release factor (eRP) 1 and eRP3. The complex can be used eukaryotic release factor (eRP) 1 and eRP3. The complex can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peltz S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide #2884.
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02-JUL-2002 ABP26966

(first entry polypeptide

ABP26966 standard;

protein; 318

۲,

Streptococcus

SEQ

ID NO 3108.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.

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                                                                                                                                                        CC microbial source. The invention also relates to a transformed plant of comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transformed plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plants with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate by modification of the cell cycle pathway with plant growth rate by modification of content, improved yield by modification of carbohydrate, nitrogen or CC content, improved yield by modification of photosynthesis or by CC providing improved lignin production or improved galactomanan or improved galactomanan or improved galactomanan or involved invention. Note: The sequence data for this pattent did not CC form part of the printed specification but was obtained in electronic format from USPTO at sequence data for this pattent did not compare the content of the printed specification but was obtained in electronic content.
                                                                              Best Local
Matches
                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                        Sequence 650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2884; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAOY/)
(HINK/)
(SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003; 2003US-00369493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GOLD/)
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      380
                                        1 VVIDEXXQAXX-XXXIPI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinkle GJ,
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VVVDEASQATIPSILIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates
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                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to a recombinant DNA na plant cell, where
                                                                                              Score 32.5;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                Mismatches
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                                                                                                                    BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  construct
                                                                                                                  8
                                                                              7;
                                                                                                                  Length 650;
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RESULT 6
ABUJ4245
ID ABUJ2
XX ABUJ2
XX ABUJ2
XX ABUJ2
XX DE Prot
XX Anti
XX Anti
XX Anti
XX Anti
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XX Y WOZC
XX WOZC
XX WOZC
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Best Local
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71556 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus agalactiae
                WO200277183-A2
                                               Mycobacterium avium
                                                                                                         Protein
                                                                                                                                          19-JUN-2003
                                                                                                                                                                       ABU34245
                                                                                                                                                                                                      ABU34245 standard; protein; 710
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 318
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N-PSDB; ABN67597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200234771-A2
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(GENO-) INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserve
                                                                                                         encoded by Prokaryotic essential gene #19772.
                                                                                                                                                                                                                                                                                  VIVDEKDOAFTNPTKPI 133
                                                                                                                                                                                                                                                                                                               VVIDEXXQAXXXXXIPI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 3464; 4525pp; English
                                                                          prokaryotic
                                                                                                                                                                                                                                                                                                                                             59.3%;
nilarity 41.2%;
Conservative
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                                                                                                                                        (first entry)
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                                                                             essential
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Pred. No. 16;
2; Mismatches
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                                                                            gene; cell proliferation; drug design
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                                                                                                                                                                                                                                                                                                                                              9,
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RESULT 7
ADN19868
ID ADN1

ADN19868 standard; protein; 1944 AA

ADN19868

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558

IMDETVQAAAADGLPL 573

2 VIDEXXOAXXXXXIPI 17

Best Loc Matches Query Match

Local

Similarity 5; Conserv

Conservative

4.

Mismatches

7;

0

Gaps

Ö

59.3%;

Score 32; Pred. No.

DB 6,

Length 710; Indels

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cc encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide by the containing the polypeptide; (5) producing the polypeptide; (6) inhibited by the continent of the polypeptide; (6) inhibiting cellular continent of the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a gene in an operon required for continent of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) continent of the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of contiferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational continuity of prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
   21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002.
                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 62169; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolate candidate molecules for rational drug
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Trawick JD,
   710
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2002US-00072851
2002US-0362699P
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2001US-00948993.
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Carr G
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
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Xu HH;
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02-DEC-2004

(first entry)

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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC such as maize or soybean. The method of producing a transformed plant CC recombinant DNA construct and growing the transforming a plant with the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of protosynthesis or by providing improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. Note: The sequence exact a bacterial polypeptide used in the corp part form uptoned the printed specification but was obtained in electronic forms part of the printed specification but was obtained in electronic condition.
                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                             Sequence 1944 AA;
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(CHEN/)
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) HINKLE G J.
) SLATER S C.
) CHEN X.
) GOLDMAN B S.
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VIIDEAAQAVELSSI 1527
                                                                         VVIDEXXQAXXXXXI 15
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                                                                                                                                                                                 59.3%;
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Query Match

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                                                                                          CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the crocombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, concerned to herbicides, extreme osmotic conditions, pathogens or pests, cc increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or content, improved plant growth and development under at least one stress cc condition, improved plant growth and development under at least one stress cc condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not compared the printed specification but was obtained in electronic features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from microbial source. The invention also relates to a transformed plant
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(HINK/)
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HINKLE G J
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GOLDMAN B
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O at seqdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                               with the 2706bp nucleic acid; a vector containing the MAA3 gene or one captured by the year, a transformed by the vector; a nucleotide containing the partial sequence of continuous 14 bases or more in the 2706bp nucleic acid or its complementary sequence; and a transforming plant with characters modified by making a female reproductive cell lethality or forming only the seed which does not contain a specific allele. The MAA3 gene is derived from Arabidopsis thaliana and is useful for making a female reproductive cell a lethality by suppressing the expression of the MAA3 gene. The MAA3 gene is useful for setting the number of seed to 1 for 2n by inserting antisense MAA3 cuse in n places of plant genome. The novel method of the invention is useful for producing transgenic plant-derived foodstuffs, which contain a forceign gene in neither a seed nor an endosperm. The MAA3 nucleotide fragment is useful as probe for detecting the MAA3 gene and is also useful for modulating the expression of the MAA3 gene. This sequence represents the 818 amino acid MAA3 protein of the invention.
                                                                                                Matches
                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         given in the specification or a sequence which has deletion, substill or addition in the amino acid(s) of the 818 amino acid protein. The invention further relates to: a gene encoding the MAA3 protein; DNA containing the MAA3 gene, as a 2706 nucleotide sequence, given in the specification or a sequence which hybridizes under stringent conditions.
                                                                                                                                                                                                                Sequence 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel magatama mutant (MAA3) protein for female reproductive cell formation, having an 818 amino acid sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel magatama mutant protein derived from Arabidopsis thaliana for female reproductive cell formation.
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transgenic; foodstuff;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               condition
                                                                                          Gaps
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                                                                                             0
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                                                                                                                                                                                                                          promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with improved plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant drowth remilators increased resistance.
                                                  of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                 scope of the invention.
form part of the printed
format from USPTO at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a recombinant DNA promoter functional in a plant cell, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial polypeptide #4012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN21359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN21359 standard; protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterial polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 VIIDEAAQA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAO Y.
HINKLE G J
SLATER S C
CHEN X.
GOLDMAN B S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4012; 122pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater
                                        seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construct comprising
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Sequence 830 AA;

Length 830;

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RESULT 11
ABO79216
                                                                                                                                                                                                                                              The invention relates to Pseudomonas aeruginosa polypeptides and the golymucleotides encoding them. The sequences are useful in diagnosis and cherapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a component of the ability to bind a P. aeruginosa nucleic acid, as components of concluding anti-P. aeruginosa drugs, as targets for antibacterial drugs, concluding anti-P. aeruginosa drugs, as templates for recombinant concluding anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-caused confection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa olypeptides of the invention. Note: The specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                             Matches
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 27962; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6551795-B1
                                                                                                                                                                                        Sequence 302 AA;
                                                                                                                                                                                                                               segdata.uspto.gov/seguence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #11391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            АВО79216;
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                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477
70
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                                                                                        l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIIDEASOA 485
WIDELLOA 78
                                            VVIDEXXQA 9
                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0074788P.
98US-0094190P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00252991.
                                                                                                                55.6%;
77.8%;
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                                                                                          0,
                                                                                                                   Score 30;
Pred. No.
                                                                                             Mismatches
                                                                                                                                         DB
                                                                                                                                         7;
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                                                                                          2
                                                                                                                                         Length 302
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                                                                                             Indels
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                                                                                             Gaps
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Query Match Best Local S Matches 6

Similarity 6; Conserva Conservative

55.6%;

Score 30; Pred. No.

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Length 352; Indels

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Mismatches DB 60;

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RESULT 12
ADB07940
ID ADB07
                                                                                          The present invention describes an isolated polynucleotide (I) of Alloicoccus otitidis genomic DNA, which encodes an antigenic protein. CC Alloicoccus otitidis is a Gram-positive bacterium. Also described: (1) CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, degenerate variant or fragment; (3) a genetically engineered complement cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, bological equivalent or fragment, or the polynucleotide that is comprising the complement polypeptide of (1); (5) an immunogenic composition vector; (6) a pharmaceutical composition comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immunising against Alloicoccus otitidis by administering to a host the containing the novel polynucleotide, its degenerate variant or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloicoccus otitidis in the biological sample; (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, cor the antibody of (4), and (1) producing a polypeptide by culturing the polypeptide from the culture. (1) can be used in gene therapy. The polynucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials. The polynucleotides are useful for expressing and detecting Alloicoccus otitidis. The present sequence represents an Alloicoccus otitidis
Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 33; SEQ ID NO 1880; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring
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18-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alloiococcus otitidis; antigenic protein; immunogenic; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alloiococcus otitis antigenic protein SEQ ID NO:1880
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                                                                         antigen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-505284/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-NOV-2002; 2002WO-US036123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH HOLDINGS CORP.
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2002US-0426742P.
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                                                                             from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zagursky
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Query Match
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"** 6; Conserve
                                                                                                                                           The present invention describes an isolated polynucleotide (I) of CC Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. CC Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polypeptide (I) and CC complement, degenerate variant or fragment; (3) a genetically engineered complement, degenerate variant or fragment; (3) a genetically engineered composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide (1); (5) an immunogenic composition vector; (6) a pharmaceutical composition comprising the expression vector; (6) a pharmaceutical composition comprising the complement, or the polypeptide of (1) a protein chip comprising an array confidency of (1) and a carrier; (7) a protein chip comprising an array confidency of (1); their biological equivalent or fragment; (8) containing against Alloiococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the novel polymucleotide, its degenerate variant or fragment, correction to the polypeptides, and (11) producing a polypeptide by culturing the correction containing the culture; (1) can be used in gene therapy. The polymucleotides polypeptides, antibodies and compositions of the present correction protein from the present sequence represents an Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis continidis contains and the correct of the present sequence represents an Alloiococcus otitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-505284/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001; 2001US-0333777P.
18-NOV-2002; 2002US-0426742P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alloiococcus otitidis; antigenic protein; immunogenic; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alloiococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB07942 standard; protein; 360 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-2003
                                                                                                                                     protein
                                                                                               360
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                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otitis antigenic protein SEQ ID NO:1882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcmichael JC,
                                                                                                                                     from the present invention.
                                   55.6%;
                Score 30; DB
Pred. No. 61;
2; Mismatches
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                                                      6
                7;
                                                      Length 360;
                Indels
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                Gaps
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CC Alloicoccus otitidis genomic DNA, which encodes an antigenic protein.
CC Alloicoccus otitidis is a Gram-positive bacterium. Also described: (1)
CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
CC expression vector comprising the novel isolated polynucleotide (1); (2) an
CC complement, degenerate variant or fragment; (3) a genetically engineered
CC composition comprising the polypeptide of (1); (5) an immunogenic
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
CC expression vector; (6) a pharmaceutical composition comprising the
CC expression vector; (6) a pharmaceutical composition comprising the
CC expression vector; (6) a pharmaceutical composition comprising the
CC polypeptide of (1) and a carrier; (7) a protein chip comprising the
CC immunogenic composition; (9) detecting and/or identifying Alloicoccus
CC containing the novel polynucleotide, its degenerate variant or fragment; (8)
CC or the antibody of (4); and (11) producing a polypeptide by culturing the
CC or the antibody of (4); and (11) producing a polypeptide by culturing the
CC polypucleotides, polypeptides, antibodies and compositions of the present
CC convention can be used for treating and diagnosing diseases, drug
CC invention sasays and monitoring of effects during and alloicocccus
CC the polymocleotides are useful for expressing and detecting Alloicocccus
CC titidis. The present sequence represents an Alloicocccus otitidis
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18-NOV-2002; 2002US-0426742P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alloiococcus otitidis; antigenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alloiococcus otitis antigenic protein SEQ ID NO:1884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated polynucleotide (I) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-505284/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in; immunogenic; immunisation; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zagursky RJ;
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Query Match Best Local Similarity

55.6%;

Score Pred.

No; 66;

6

Length 385;

Sequence

385

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RESULT 15
ADB07946
ID B07946
AC ADB07946
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                                                           The present invention describes an isolated polynucleotide (I) of CC Allolococcus otitidis genomic DNA, which encodes an antigenic protein. CC Allolococcus otitidis is a Gram-positive bacterium. Also described: (1) CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an isolated polynucleotide (I); (2) an isolated polynucleotide (I); (3) an isolated polynucleotide (I); (5) an isolated complement, degenerate variant or fragment; (3) a genetically engineered complement, degenerate variant or infected with the vector of (2); (6) host cell, transformed or infected with the vector of (2); (7) an isolated polynucleotide (I); (5) an isolated in the composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polynucleotide that is comprised in the CC expression vector; (6) a pharmaceutical composition comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) (8) immunising against Allolococcus otitidis by administering to a host the containing the biological sample; (10) a kit comprising a container containing the novel polynucleotide, its degenerate variant or fragment, cromatining the novel polynucleotide, its degenerate variant or fragment, comprising and the polypeptide from the culture. (I) can be used in gene therapy. The comprision can be used for treating and diagnositions of the present container may be polynucleotides, polypeptides, antibodies and compositions of the present continues of the present sequence represents an Allolococcus otitidis outlides on the container of the present invention.
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18-NOV-2002; 2002US-0426742P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Russell DP, Zagursky RJ;
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Sequence 388 AA

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                                  Best Local Similarity
Matches, 6; Conserv
                                                    Query Match
136 LDELNOASADLGLPI 150
                 3 IDEXXOAXXXXXIPI 17
                                   Conservative
                                            55.6%;
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                                             Score 30; DB
Pred. No. 67;
                                    Mismatches
                                                      6
                                    7;
                                                      Length 388;
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Job time : 85.7389 secs

Search completed: April 18, 2005, 08:03:44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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DB
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54
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length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 100%
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          US-09-359-268A-3
US-09-902-540-1354
US-09-902-540-1962
US-09-928-796A-20994
US-09-248-796A-29
US-09-352-991A-17847
US-09-352-991A-11693
US-09-920-540-11693
US-09-9170-984A-22
US-09-177-431-8
US-09-177-431-8
US-09-177-431-9
US-09-178-354D-9
US-09-278-354D-9
US-09-278-354D-9
US-09-278-354D-4
US-09-278-354D-4
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US-09-278-354D-4
US-09-278-354D-4
US-09-278-354D-2
US-09-278-384B-2
US-09-278-384B-2
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Compugen Ltd.
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Sequence 13564, A
Sequence 27962, Ap
Sequence 1100, Ap
Sequence 20994, A
Sequence 17847, A
Sequence 2529, Ap
Sequence 2529, Ap
Sequence 17693, Ap
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22, Appl
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19347, A
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US-09-359-268A-3
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Sequence 18, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 7716, Ap	Sequence 48311, A		Sequence 6413, Ap	•	Sequence 483, App	Sequence 6578, Ap	Sequence 26, Appl	Sequence 2, Appli	Sequence 28, Appl	۲	Sequence 538, App	Sequence 9913, Ap	Sequence 2, Appli

ALIGNMENTS

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Sequence 13544, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FITLE OF INVENTION: Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                              RESULT 2
US-09-902-540-13564
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APPLICANT: Czaplinaki, Kevin
APPLICANT: Czaplinaki, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPAMILY OF RNA HELIC
TITLE OF INVENTION: THE FIDELITY OF TRANSLAT
TITLE OF INVENTION: THEROP
FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
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Best Local S
Matches 17
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SEQ ID NO 3
LENGTH: 17
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Saccharomyces cerevisiae FEATURE:
OTHER INFORMATION: Xaa = any amino acid
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RESULT 4
US-09-538-092-1100
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US-09-538-092-1100
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US-09-902-540-13564
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SEQ ID NO 1364
LENGTH: 513
TYPE: PRT
                                                                                                                                    PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.
SEQ ID NO 1100
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NUMBER OF SEQ ID NOS:
SEQ ID NO 27962
LENGTH: 302
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Patent No. 6551795
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Best Local
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APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
CURRENT FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION 1998-07-27
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TITLE OF INVENTION:
TITLE OF INVENTION:
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PRIOR APPLICATION NUMBER: US 60/074,788
     NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P38935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                      FEATURE:
                                                                                    ORGANISM: Homo sapiens
                                                                                                         TYPE: PRT
                                                                                                                       ENGTH: 993
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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77.8%;
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Pred. No.
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Pred. No. 26;
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17847
LENGTH: 161
TPB: PRT
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Best Local Similarity
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US-09-252-991A-17847
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Best Local Similarity 37.5%;
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                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 28208
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Keith Weinstock et al
                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILE REFERENCE: 107196.132
                                                                             Local
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                                                                             Score 29; DB Pred. No. 24;
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Pred. No.
                                                              Mismatches
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                                                                                              Length 161;
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                                                                                                                                                                                                                                           US-09-902-540-11693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: M.catarrhalis
US-09-540-236-2529
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SEQ ID NO 29
LENGTH: 380
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFITITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2529
LENGTH: 413
TYPE: PRT
                                                                                                                                                                                            Sequence 11693, Ap
Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.7%; Score 29; DB Best Local Similarity 31.2%; Pred. No. 63; Matches 5; Conservative 3; Mismatches
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APPLICANT:
APPLICANT:
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TIPLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: saccharomyces cerevisiae
                                                                                                                                                                            INFORMATION:
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Czaplinski, Kevin
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66.7%;
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Pred. No. 58;
1; Mismatches
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RESULT 11 US-09-270-984A-22

Sequence 22, Application US/09270984A Patent No. 6048965
GENERAL INFORMATION:

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US-08-724-354D-22
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                                                                                                                                  US-08-724-354D-22
                                      Query Match
Best Local Similarity 66...
""" hes 6; Conservative
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NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11693
LENGTH: 671
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: 60/016,482
PRIOR APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 59941:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dietz,
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                               NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 077
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                  TOPOLOGY:
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569 VLÍDESTÓA 577
                             1 VVIDEXXQA 9
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Pred. No. 1e+02;
                                                                                 Score 29; DB 2;
Pred. No. 1.5e+02;
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US-09-177-431-8
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Patent No. 6071700
GENERAL INFORMATION:
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APPLICATION NUMBER: US/
FILING DATE:
PRIOR APPLICATION NUMBER: 08/
APPLICATION NUMBER: 08/
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                        APPLICANT: He, Feng
APPLICANT: Jacobson,
TITLE OF INVENTION: I
               FILING DATE:
PRIOR APPLICATION DATA:
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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 APPLICATION NUMBER:
                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                         CITY: Boston
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                                              APPLICATION NUMBER:
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VENTION: MAMMALIAN REGULATOR OF
VENTION: NONSENSE-MEDIATED RNA DECAY
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FastSEQ for Windows Version
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HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
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66.7%;
08/955,472
                                             US/09/177,431
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Pred. No. 1.5e+02;
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US-08-724-354D-9
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US-09-248-796A-19347
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                             Sequence 9, Application US/08724354D Patent No. 5994119
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LENGTH: 917
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: FASBE, J. PECET
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                    TITLE OF INVENTION: MATTITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 53.7%;
Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
COUNTRY:
                                                 ADDRESSEE: Fish & Richardson, P.C. STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569 VLÍDESTOA 577
                                                                                                                                                                                                                                                                                                             619 VIIDEATOSSEPTTLIPL 636
                                                                                                                                                                                                                                                                                                                                                  1 VVIDEXXQAXX-XXXIPI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VVIDEXXQA 9
                 La Jolla
CA
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617/542-9806
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                                                                                                                                                                                                                                                                                                                                                                                                     52.8%;
                                                                                                                            NONSENSE-MEDIATED
                                                                                                                                               MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 28.5; DB 4;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 3;
Pred. No. 1.5e+0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                              RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5e+02;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

92037

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-724-354D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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US-09-270-984A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.9%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09270984A Patent No. 6048965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
PILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                          ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-578-5070
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: Wil
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,354
                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,984A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
                                                                                                                                                                                                   FILING DATE:
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IBM Compatible
SYSTEM: Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 28; DB 2; Pred. No. 7.1; 2; Mismatches
                                                                                                            07265/090001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-270-984A-9
Search completed: April 18, 2005, 08:18:33 Job time: 22.219 secs
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                                                                                Query Match
Best Local Similarity
Watches 5; Conserve
                                                                                                                                                                              TYPE: amino acid
                                                1 ILIDESTOA 9
                                                                      1 VVIDEXXQA 9
                                                                                             Conservative
                                                                                                         51.9%;
                                                                                             Score 28; DB 3;
Pred. No. 7.1;
2; Mismatches
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                                                                                                                    Length 30;
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No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
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Match
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54
1 VVIDEXXQAXXXXXIPI
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*
/ Cgn2 6/ptodata/1/pubpaa/US10 PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2 6/ptodate/1/pubpaa/USO7 PUBCOMB.pep:*
/cgn2 6/ptodate/1/pubpaa/PCT NEW_PUB.pep:*
/cgn2 6/ptodate/1/pubpaa/USO6 NEW_PUB.pep:*
/cgn2 6/ptodate/1/pubpaa/USO6 PUBCOMB.pep:*
/cgn2 6/ptodate/1/pubpaa/USO7 NEW_PUB.pep:*
/cgn2 6/ptodate/1/pubpaa/PCTUS PUBCOMB.pep:*
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              US-10-652-334-3

US-10-437-963-111797

US-10-437-963-111794

US-10-369-493-2884

US-10-369-493-2884

US-10-425-114-38637

US-10-425-114-38637

US-10-425-114-37833

US-10-282-122A-62169

US-10-369-493-2521

US-10-437-963-140079

US-10-437-963-140079

US-10-424-599-252174
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                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                       Sequence 3, 1
Sequence 111:
Sequence 111:
Sequence 498:
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Sequence
Sequence
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Sequence
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                    49859, A
2884, Ap
38637, A
38633, A
62163, A
2521, Ap
140079,
57601, A
252174,
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111797,
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Sequence 173736,	ű		8 51.	
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e 27, App	US-10-165-		8 51.	
quence 2	US-09-910	377	28 51.9	
46769,	US-10-282-122A-4		8 51.	
equence 67195,	US-10-282-122		8 51.	
Sequence 45661, A	US-10-282-122A-4		8 51.	
1216,	US-10-369-492		8 51.	
e 17089,	US-10-369-493-1708		8 51.	
71299,	US-10-425-114-		8 51.	
1864	US-10-424-599-1864		8 51.	
Sequence 2087, Ap	US-10-369		9 53.	
equenc	US-10-424-599-20564		9 53.	
	US-10-437		9 53.	
equenc	US-10-652-		9 53.	
equence	US-10-282-122A-472		9 53.	
Sequence 38822, A	US-10-767-701-3882		9 53.	
Sequence 21357, A	US-10-369		.5 54.	29
	US-10-437-963-1852		0 55.	
19514	US-10-424		0 55.	
21435	US-10-369-493-2		0 55.	
Sequence 37557, A	US-10-425-114-3755		0 55.	
	US-10		0 55.	
equence 41078,	US-10-767-701-		0 55.	
equence	US-10-369-493-		0 55.	
e 10407,	US-10-156-761		0 55.	
Φ	US-10-424-599-		0 55.	
e 4012	US-10-369-493-		٠	
e 22762,	US-10-369-493		1 .57.	
Sequence 37717, A	US-10-425-114-3		_	
233	-424-599-	637	31 57.4	15
Sequence 166322,	US-10-437-963-1		31 57.4	14

ALIGNMENTS

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US-10-652-334-3
                                                                       Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10652334 Publication No. US20040115787A1
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLS OF INVENTION: A SUBRAMILY OF RNA HELICASES
TITLS OF INVENTION: THE FIDELITY OF TRANSLATION
TITLS OF INVENTION: THEREOF
FILE REPERENCE: 601-1-85N
                                                                                                                                                                  OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                   ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                               PEATURE:
                                                                                                                                                                                                                                         LENGTH:
 \vdash
                                                                       l Similarity
17; Conser
                         VVIDEXXQAXXXXXIPI
                                                                     74.1%; Score 40;
larity 100.0%; Pred. No.
Conservative 0; Mismatci
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US-10-437-963-111794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_15741C.1.pep
US-10-437-963-111797
                                                                                                                                                                                                                                    CURRENT FILING DATE: 2003-0.
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 111794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 111794, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: La Roba, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 111797, Application US/10437963 Publication No. US20040123343A1
Query Match
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LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Flance Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                          NAME/KEY: unsure
LOCATION: (1)..(1323)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(256)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                            ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
                                                          OTHER INFORMATION: Clone ID: PAT_MRT4530_15739C.1.pep
                                                                                                                                                                                                                        ENGTH: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 70.4%;
Local Similarity 50.0%;
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Barbazuk, Brad
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  70.4%;
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  Score 38;
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  DB 16;
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  Length 1323;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2884
LENGTH: 650
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US-10-369-493-2884
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US-10-767-701-49859
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US-10-767-701-49859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2884, Application US/10369493 Publication No. US20030233675A1
                                                                                          Best Local Similarity
                                                                                                           Query Match
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Best Local
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APPLICANT: Zhou, Y
APPLICANT: Cao, Yo
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ORGANISM: Sorghum bicolor
                                                                                                                                                                  ORGANISM: Thermotoga maritima
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380
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                                 1 VVIDEXXQAXX-XXXIPI 17
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8; Conserv
VVVDEASQATIPSILIPI 397
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Cao, Yongwei
                                                                          Conservative
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                                                                                          50.0%;
                                                                                            Score 32.5;
Pred. No. 4:
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Pred. No. 0.
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                                                                                              42;
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                                                                                                             Length 650;
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                                   US-10-282-122A-62169
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                                                    RESULT 8
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Sequence 62169, Application US/10282122A
Publication No. US20040029129A1
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SEQ ID NO 37933
LENGTH: 404
TYPE: PRT
ORGANISM: Zea maye
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Best Local
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LENGTH: 332
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Best Local
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APPLICANT:
APPLICANT:
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Publication No. US20040034888A1
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Publication No. US20040034888A1
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
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                                                                                                                                                                                                                                                                   PEATURE:
OTHER INFORMATION: Clone ID:
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ORGANISM: Zea mays
FEATURE:
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                                                                                                         VVIDEAAQA 138
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Kovalic, David K.
Screen, Steven B
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Pred. No.
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Pred. No. 33;
0; Mismatches 2
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                        Sequence 2521, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US(10/369,493) CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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PRIOR APPLICATION NUMBER: 60/
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5; Conserv
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Zyskind, Judith
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Haselbeck, Robert
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31.2%; Pred. No.
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62;
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; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2521
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US-10-767-701-57601
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                                                                                                                                                              TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 57601
                                                                                                                                                                                                                                                                                                                                                        Sequence 57601, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
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Matches 7; Conserv
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SEQ ID NO 140079
LENGTH: 1975
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Publication No. US20040123343A1
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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CURRENT FILING DATE: 2003-05-14
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                                    NAME/KEY: unsure
LOCATION: (1)..(219)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                          ORGANISM: Sorghum bicolor
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INFORMATION: Clone ID: 30969562.pep
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Similarity 46.7%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                       David K.
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77.8%;
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Pred. No. 2e+02;
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Pred. No. 2e+02;
D; Mismatches
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; OTHER INFORMATION: Clone US-10-437-963-190072
                                                                                                    APPLICANT: Li, Ping, TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; PILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190072
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US-10-424-599-252174
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 252174
LENGTH: 262
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic David K
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LOCATION: (1)..(262)
OTHER INFORMATION: unsure at all Xaa locations
                                  ORGANISM: Oryza sativa FEATURE:
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                                                                                      LENGTH: 559
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66.7%;
                 ID: PAT_MRT4530_8651C.1.pep
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Pred. No.

    Mismatches

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RESULT 15
US-10-424-599-233501
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US-10-437-963-166322
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US-10-437-963-166322
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey I
                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233501
LENGTH: 637
TYPE: PRT
ORGANISM: Glycine max
PEATURE:
                                                                                                                                                                                                                                                                                                                                                               Sequence 233501, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Best Local (
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SEQ ID NO 166322
LENGTH: 626
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Best Local Similarity 66.7%;
Matches 6; Conservative
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CURRENT FILING DATE: 2003-05-14
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NAME/KEY: unsure
LOCATION: (1)..(626)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Oryza sativa
NAME/KEY: unsure
LOCATION: (1)..(637)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 57.4%; Score 31; DB 16; Length 626; Local Similarity 66.7%; Pred. No. 95; hes 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 VIIDEAAQA 361
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Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
Li, Ping
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Pred. No. 84;
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Search completed: April 18, Job time: 61.3066 Becs

2005, 09:04:06

This Pogo Blonk (Usoro)

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Result
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A;Cross-references: UNIPROT:P47386; GB:U39694; GB:L43967; NID:g1045822; PID:g1045823; TIO:g1045823; TIO:g10458235; TIO:g10458235; TIO:g10458235; TIO:g10458235; TIO:g10458235; TIO:g10458235; TIO:g10458235; TIO:g10

A; Molecule type: DNA A; Residues: 1-1113 < TIGR>

M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; I. (C.A.; Venter, J.C. Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium. A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64215

A; Status: preliminary; nucleic acid sequence not shown; translation not

hypothetical protein MG140 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: E64215; S18694
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleis

.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R. D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick,

R.D.; ck, J.

E64215

ALIGNMENTS

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A; Molecule type: DA
A; Residues: 1-1113 <HIM>
A; Cross-references: UNITROT: P75033;
A; Note: the nucleotide sequence was C; Genetics:
                                                                                                                                                     R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasm A;Reference number: S73327, MUID:97105885; PMID:8948633
A;Accession: S73327
A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
                                                                                                                                                                                                                                                                                            C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
A;Variety: 26-Fe__1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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                                      A; Genetic code:
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N;Alternate names: hypothetical protein E07_orf1113
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Pred. No. 0.35;
0; Mismatches
Score 39;
                                                                             EMBL:AE000001; GB:U00089; NID:g1673645; PIDN:AAB9564 submitted to the EMBL Data Library, November 1996
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C;Accession: T08986
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16520
A;Accession: T08986
A;Molecule type: DNA
                                                                                                                                                                                                                                                                          A;Residues: 1-1311 <BEV>
A;Residues: 1-1311 <BEV>
A;Cross-references: UNIPROT:Q9SZW3; EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.130
A;Cross-references: Cultivar Columbia; BAC clone F6G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F6G3.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A;Reference number: Z14167
A;Recession: T00533
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A;Accession: G84572
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;Molecule type: DNA
;Residues: 1-1090 <STO>
;Residues: GB:AE002093;
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"Experimental source: cultivar Columbia
"Experimental source: Columbia, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.; Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, U.S.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Uss, D.; Venter, W.C.; White, O.; Eisen, D.; Venter, W.C.; White, O.; White, O.; Eisen, D.; Venter, W.C.; White, O.; White, O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: DNA
;Residues: 1-1090 <ROU>
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                                                                                                                                                                                            Map position:
                                                                                                                                                                                                                                                                      Genetics:
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Matches 9; Conservative
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Best Local (
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                                                                              Query Match
                                                                                                                                                                                                                                   Gene: ATSP:F6G3.130
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                                                                                                                                                        414/1;
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   Similarity
8; Conserv
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68.5%;
nilarity 50.0%;
Conservative :
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llarity 50.0%;
Conservative
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                                                                                                                                                        506/1; 547/2; 591/3; 1179/3
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Pred. No. 1.1;
1; Mismatches 7; Indels
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   Score 37; DB 2; Length 1311; Pred. No. 1.3; 1; Mismatches 7; Indels
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0; Mismatches
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Έ
                                                                  r17F16:1 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86303
                                           R;Theologis,
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   Chin,
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A;Gene:
A;Map po
                                                                                                                                                                                                                                                                                                                                                             TRNA-splicing endonuclease positive effector - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T40065 C;Accession: T40065 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F. submitted to the EMBL Data Library, December 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: TM0005
C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;ReBidueB: 1-650 <ARN>
A;Cross-references: UNIPROT:Q9WXM0; GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD35099A; A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Evidence for lateral gene transfer between Archaea and A,Reference number: A72200; MUID:99287316; PMID:10360571 A,ACCESSION: G72429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 C;Accession: G72429
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A;Cross-references: UNIPROT:O94387; EMBL:AL034463; PIDN:CAA22438.1; GSPDB:GN00067; SPDB:E
A;Experimental source: strain 972h-; cosmid c29A10
                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T40065
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                                                                                                 Query Match
Best Local
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Best Local
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                                                                              Matches
                                                                                                                                                            position:
                                                                                               Local
                                                                                                                                                              SPDB:SPBC29A10.10c
osition: 2
1513 VIIDEAAQAVELSSI 1527
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                                                                                                 Similarity
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                                      VVIDEXXQAXXXXXI 15
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                                                                                Conservative
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                                                                                                 59.3%;
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Pred. No. 37;
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A.; Ecker, J.R.; Palm, Chung, M.K.; Conn, L.; Hughes, B.; Huizar, L.

C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                          hypothetical protein - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71420
C;Accession: E71420
R;Bevan, M, Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdomenech
a;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Benes, V.; Rechman, S.; Ans
C; Challastia N.
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A;Residues: 1-2142 <STO>
A;Cross-references: UNIPROT:Q9FWR3; GB:AE005172; NID:g9954728; PIDN:AAG09081.1; GSPDB:GN
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A; Residues: 1-530 <AQF>
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                                         A,Reference number: A71400;
A,Accession: E71420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                          A, Title: Analysis of 1.9 Mb
                                                                                                                C.; Chalwatzis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
;Accession: D70476
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preliminary;
e type: DNA
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                   nucleic acid sequence not
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77.8%;
                                                                  of contiguous sequence from MUID:98121113; PMID:9461215
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Pred. No. 16;
1; Mismatches
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Pred. No. 41;
0; Mismatches
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16;
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RESULT 10
T41580
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A; Cross-references: UNIPROT: Q92355; EMBL: Z81317;
A; Cross-references: strain 972h-; cosmid c6G9
                                                                                                                                                                                                                                                                                                                                    DNA2-NAM7 helicase family protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #secrips-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-555 <BEV>
A;Cross-references: UNIPROT:023408;
C;Genetics:
A;Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable dna-binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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A; Accession: T39072
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A;Introns: 14/3; 72/2; 151/2
C;Superfamily: probable DNA helicase MJ0104
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A;Molecule type: DNA
A;Residues: 1-660 <MUR>
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                                                                                                                                                                                                                                                                                                                     C; Accession: T39072
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A;Experimental source: strain 972h(-)
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A; Accession: T41580
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                              1 VVIDEXXQA 9
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                                                             Similarity 6; Conser
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VIIDEAAQA 1383
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66.7%;
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                                                             Score 31; DB Pred. No. 57; Mismatches
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Pred. No.
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Pred. No.
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RESULT 12

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C;Accession: B83395
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey,
                                                                                                                      probable helicase At2903270 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T18E12.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02699; D84446
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                           A;Description: Arabidopsis thaliana chromosome A;Reference number: Z14702
                                                                           R;Rounsley, S.D.; Lin, X.; Kaul, S. submitted to the EMBL Data Library,
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C;Species: Bacillus halodurans
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A;Cross-references: UNIPROT:Q91298; GB:AE004627; GB:AE004091; NID:g9948007; PIDN:AAG0540
A:Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: B83395
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                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9K625; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07
A;Experimental source: strain C-125
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A; Residues: 1-395 < STO>
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Best Local
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T02699
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                                                                                               X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen,
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77.8%;
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K.; Lim,
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Search completed: April 18, Job time: 17.3796 secs

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A;Cross-references: UNIPROT:081047; EMBL:AC005313; NID:g3548797; PID:g3548803
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable DNA helicase MJ0104 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep_196 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64312
C;A
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H64312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus ja A;Reference number: A64300; MUID:96337999; PMID:8688087 A;Accession: H64312
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A;Residues: 1-635 <STO>
A;Cross-references: GB:AE002093; NID:g4335770; PIDN:AAD17447.1; GSPDB:GN00139
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-635 <ROU>
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A;Map position: 2
C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                                                                              A;Start codon:
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: FOR99243-101234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-663 <BUL>
A;Cross-references: UNIPROT:Q57568; GB:U67467; GB:L77117; NID:g2826242; PIDN:AAB98084.1;
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66.7%;
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jannaschii
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Maximum Match 100%
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Maximum DB seq
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Perfect score:
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
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SWISS- en th uropea by no ied an ies re dies re 03969 X6151 U0174	SEQUINCE OF 206- STRAIN-ATCC 3353 MEDLINE-92051396 Peterson S.N., 9 "A random sequer of Mycoplasma 96 Nucleic Acids Re S[3] S[3] S[3] S[3] S[3] S[3] S[3] S[3]	NCE FRONN=ATCC NN=9601 r C.M. chmann hman J n D.T. JF., son S.1 miniman miniman ce 270	MYCGB 6; Q49; 8-1996 B-1996 T-2004 T-2004 hetica. edLocu. lasma (Tria; F;	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
the Swiss I pean Bioinfo non-profit and this strequires a san email to email to 25.2; CAA4311729; AAC13	SEQUENCE OF 206-267 STRAIN-ATCC 33530 / MEDLINE-92051396; P Peterson S.N., Schr "A random sequencin of Mycoplasma genit Nucleic Acids Res. [3] SEQUENCE OF 128-267 STRAIN-ATCC 33530 / MEDLINE-94075230; P Peterson S.N., Hu P Peterson S.N., Hu P "A survey of the My sequencing."; J. Bacteriol 175:7 -i- SIMILARITY: Bel	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=ATCC 33530 / G- MEDLINE=96026346; Pubm MEDLINE=96026346; Pubm Praser C.M., Gocayne J Pleischmann R.D., Bult Pritchman J.L., Weidman Myuyen D.T., Utrerback Tomb J.F., "Dougherty Peterson S.N., Smith H Peterson S.N., Smith H Peterson S.N., Smith H Science 270:397-403(19) [2]	STA (Rel. (Rel. (Rel. (Rel. ATP-L NAMMES= genital irmicut 2097;	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
OT entry is compared to the co	PubMe ramm ng ag taliu taliu 19:6	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=ATCC 33530 / G-37; MEDLINE=96026346; PubMed=7569 Praser C.M., Gocayne J.D., Wh Fleischmann R.D., Bult C.J., Fritchman J.L., Weidman J.F., Mryuyen D.T., Utterback T.R., Mryuyen D.T., Utterback T.R., Bromb JF., Dougherty B.A., B Peterson S.N., Smith H.O., Hu "The minimal gene complement Science 270:397-403(1995).	STANDARD; Q49283; Q4944 al. 33, Creates al. 35, Last so bl. 45, Last ar PP-binding prot mes=MG140; Italium. Icutes; Mollicu	402 420 426 639 648 663 993 1034
nnethuco naettato	M N.A. cd=1945 N. Hu proach m."; 027-60 4-394 3-194 3-194 8-8253 Bott asma g	-37; Med=756 J.D. W t C.J., an J.F. k T.R., B.A., B.A., H.O., H plement	Q49 eat eat pr	00100100000000
pyright. It is produced te of Bioinformatics and Institute. There are no utions as long as its cois not removed. Usage agreement (See http://www.gisb-sib.ch).	A. A5886; Hu PC., Bott K.F., Hutchison the process of the placing markers on the process of the placing markers on the process of the process of the process of the DNA2/NAM7 helicase family.	3; e O., Adams M.D., Cl rlavage A.R., Suttor mall K.V., Sandusky M., Phillips tt K.P., Hu PC., Lu hison C.A. III, Vent Mycoplasma genital	RT; 1113 AA. Q49472; lence update) tation update) n MG140.	Q7VKG3 Q62WG2 Q63XA8 Q6CV89 Q6CV89 Q9FXX9 Q18479 Q18479 Y104 METJA Q6YVT6 Q7R8F5 SMB2 HUMAN Q7P6Q0 ALIGNMENTS
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collaboration L outstation - ctions on its s in no way for commercial b.ch/announce/	Bical map	R.A., Kelley J.M., Ermann J.L., Merrick J.M., S.,	na .	haemophilus burkholderi burkholderi kluyveromyc streptomyce arabidopsis caenorhabdi methancocc oryza sativ plasmodium homo sepien photorhabdu fusobacteri

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Q8W5K9;
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Putative DNA
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PIR; E64215;
TIGR; MG140;
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical ATP-binding protein MG140 homolog
OrderedLocusNames=MPN153; ORFNames=MP001;
                                                                                                                                                                                                          NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                               ATP-binding;
                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.";
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Bacteria; Firmicutes;
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P75033;
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E64215; E64215.
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e DNA2-NAM7 helicase
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family protein.
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D -> R (in Ref. 2 and 3).

L -> W (in Ref. 3).

PIGVISKIR -> QLGWFLKSD (in Ref. MW; FF0C51F926725D3F CRC64;
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RESULT 5 064476

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064476; 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2003 (TrEMBLrel. 24, Putative DNA2-NAM7 helicase

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RESULT
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Q7XH59;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                             GO; GO:0004386; F:helicase activity; Helicase.
SEQUENCE 1468 AA; 163521 MW; B611
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The Rice Chromosome 10 Sequencing Consortium;
and evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=OSJNBa0079B05.7;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Wing R.A., Yu Y., Soderlund C., Chen M., Kim H
Wang R.A., Henry D., Oates R., Simmons J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; AC079179; AAL31652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "In-depth view of structure, chromosome 10.";
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
Putative DNA2-NAM7 helicase
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                    Gramene; Q7XH59; -
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Helicase.
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                                                                                                                                                 Length 1468;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 12, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F6G3.130 (Hypothetical protein AT4g30100)
Name=F6G3.130; Synonyms=AT4g30100;
                                                                                                                                                                          EU Arabidopsis sequencing proj
Submitted (MAR-2000) to the EM
EMBL; AL078464; CAB43845.1; -.
EMBL; AL161576; CAB81003.1; -.
PIR; T08986; T08986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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Mayer K.F.X., Lemcke
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Brandon R.C., Sykes S.M., Mason
Somerville C.R., Venter J.C.;
Submitted (MAR-2000) to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                  SEQUENCE
                                                                                                                                                         Hypothetical
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8; Conserv
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  VVIDEXXQAXXXXXIP 16
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                                                                                                                                il protein.
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to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                 project;
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                                                                  Score 37;
Pred. No.
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T.M., Kerlavage A.R., Adam
                                                                                                                                  0F430B9EB3A02AA4 CRC64;
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RESULT 8
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Best Local
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Q86AS0;
01-JUN-2003.
01-JUN-2003
                                                                                                                            MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dea Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Ku Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., N "Sequence and analysis of chromosome 2 of Dictyostelium dis
                                                                                                                                                                                                                                                                                                                                                                          Similar to Neurospora crassa. Related to SENI protein. Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22297686; PubMed=12368813; DOI=10.1038/nbt749; Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J., Daugherty S.C., DeBoy R.T., Dodgon R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Uterback T.R., McDonald L.A., Fraser C.M.; Venter J.C., Nealson K.H., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                      SEQUENCE FR
STRAIN=AX4;
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Complete proteome; Hypothetical protein.
SEQUENCE 907 AA; 101616 MW; EB2D0DDD9EB553
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Nat. Biotechnol. 20:1118
                                                                                                        Nature
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=44689;
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                                                   FROM
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Pred. No.
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Guigo R., Kumpf K.,
senthal A., Noegel A.A.;
yostelium discoideum.";
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EMBL; AE016967; AAP56445.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004003; F:ATP-dependent DNA he
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR000212; UvrD-helicase.
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SEQUENCE
                             SEQUENCE FROM N.A. STRAIN=F7;
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Stakenborg T.,
                                                                                                                             NCBI_TaxID=2099;
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Bacteria; Firmicutes; Mol
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01-NOV-1999 (TrEMBLrel. 12, L
01-MAR-2004 (TrEMBLrel. 26, I
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01-MAR-2004 (TrEMBLrel.
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GO; GO:000367; F:DNA binding; GO;
GO:00034386; F:helicase activity;
InterPro; IPR004483; put_DNA helic.
TIGREPAMS; TIGR00376; put_DNA helic;
Complete proteome; Helicase.
SEQUENCE 650 AA; 74241 MW; 9378FE
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STRAIN=MSB8 / DSM 3109 / ATCC 43589;

MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;

MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
                               NCBI_TaxID=216466;
                                                   Streptococcus
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                                                                                                                          Carbamate kinase.
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                                                                        iae (serotype V).
Lactobacillales; Streptococcaceae;
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Last sequence update)
Last annotation updat
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                               Score 32.5;
Pred. No. 59;
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GO; GO:0008652; F:amino acid biosynthesis; IEA.
GO; GO:0006525; F:arginine metabolism; IEA.
InterPro; IPR001048; Aa kinase.
InterPro; IPR003964; Bac_carb_kinase.
Fiam; PF00696; AA kinase; 1.
PIRSPO0773; Carbamate kin; 1.
PRINTS; PR01469; CARBMTKINASE.
TIGRPAMS; TIGR00746; arcC; 1.
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GO; GO:0008804; P:carb
GO; GO:0008652; P:amin
GO; GO:0006525; P:argi
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=22242508; PubMed=12354221;
MEDLINE=2242508; PubMed=123542508; PubMed=125
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Q8E2J6;
01-MAR-2003
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MEDLINB=22222988, PubMed=12200547; DOI=10.1073/pnas.182380799;

Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.!

Wessels M.R., Paulsen I.T., Nelson K.B., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora

Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.MAR-2003 (TrEMBLrel. 23, Created)
01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2004 (TrEMBLrel. 26, Last annotation updat)
Hypothetical protein gbs2126.
                                                              GO; GO:0008804; F:carbamate kinase activity; IE GO; GO:0008652; F:amino acid biosynthesis; IEA. GO; GO:0006525; F:arginine metabolism; IEA. InterPro; IPR001048; Aa kinase. InterPro; IPR003964; BaC Carb Kinase. Pfam; PF00696; AA kinase; 1. PFam; PF00696; AK kinase. Pfam; PF00696; AK kinase. Pfam; PF00696; AK kinase.
                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Streptococcus invasive neonatal disease."; Mol. Microbiol. 45:1499-1513(2002) EMBL; AL766856; CAD47785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=216495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=gbs2126;
Streptococcus agalactiae (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR;
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                                                                                                                                                                                                                                                                                                                                                                           HSSP; P35836; 1878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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34006 MW;
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Lactobacillales; Streptococcaceae;
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Pred. No. 38;
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C., Trieu-Cuot P.,
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Matches 7
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Q6AQT5;
25-OCT-2004 (TrEMBLrel. 28, 0
25-OCT-2004 (TrEMBLrel. 28, 1
25-OCT-2004 (TrEMBLrel. 28, 1
Probable acetate kinase.
Name=SPBC27A1..... Schizosaccharomyces pombe (Fission year... Schizosaccharomyces pombe (Fission year... Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
                                                                                                                 SPBC29A10.10c prote
Name=SPBC29A10.10c;
                                                                                                                                                                      01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRPAMS; TIGRO0016; AckA; 1.

PROSITE; PS01075; ACETATE KINASE 1; 1.

PROSITE; PS01076; ACETATE KINASE 2; 1.

Complete proteome; Kinase; Transferase.

SEQUENCE 405 AA; 44128 MW; ED790BC
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Bauer M., Zibat A.,
Teeling H., Leuschn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00871; Acetate kinase; PRINTS; PR00471; ACETATEKNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15305914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro; IPR004372; AckA.
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown D., Brown S., Chillingworth T., Churcher C.,
RA Brown B., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Gilier K., Jones M., Squares R., Squares S., Stevens K.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Moodward J., Vanstreels B., Rleger M., Schafer M., Muller-Auer S.,
RA Welljens I., Vanstreels B., Rleger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Leharch W., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT Tenger A., Revuelta J.L., McCombie W.R., Paulsen I., Potashkin J.,
REMBL; AL034463; CAA22438.1; -.

DR EMBL; A1034463; CAA22438.1; -.
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InterPro; IPR000B73; AMP-bind.
PROSITE; PS00455; AMP BINDING; UNKNOWN 1.
SEQUENCE 1944 AA; 222209 MW; 12B005A934BEE11C CRC64;
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ALIGNMENTS

RESULT 1 ABW01180 ID ABW0 Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast. Saccharomyces cerevisiae motif IV peptide WPI; 2003-810549/76. Peltz S, 22-JUL-1998; 07-OCT-2003. US6630294-B1. Misc-difference Misc-difference Misc-difference Misc-difference Saccharomyces cerevisiae. 15-JAN-2004 (first entry) ABW01180; ABW01180 standard; peptide; 12 (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY 22-JUL-1999; Czaplinski K, 98US-0093685P. 99US-00359268 Location/Qualifiers /label= Unknown /note= "Xaa may /note= "Xaa may /note= "Xaa may be 'label= Unknown note= label= Unknown note= "Xaa may label= Unknown Dinman ጅ £, þe be þe any any any any amino amino acid" amino amino acid" acid" acid"

Identifying an agent that increases nonsense suppression, for anti-therapy, by contacting modulator of translation termination (Mtt1) Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mtt1.

for antiviral

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Disclosure;

Col 43-44;

Opp; English.

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                                                                                                                                                                                                                                                                                                                        (PELT/)
(CZAP/)
(DINM/)
                                                                                                  Identifying a test composition or agent that translation termination comprises contacting composition or agent, and determining if the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer;
                              Claim 36;
                                                                                                                                                                                                                  WPI; 2004-449400/42
                                                                                                                                                                                                                                                                       Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast translation termination modulation protein motif IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP44106 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                     ) PELTZ S.
) CZAPLINSKI K.
) DINMAN J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 100
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                                                                                  the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AA;
                                                                                                                                                                                                                                                                    Czaplinski K,
                              SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003US-00652334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0093685P.
99US-00359268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%; but
100.0%; Pr
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                                4.
                              41pp; English
                                                                                                                                                                                                                                                                       Dinman
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b; Pred. No. 0.1
0; Mismatches
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0.13;
                                                                                                        modulates the efficiency of
the MTT1 with the test
test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-globin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>۰</u>
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RESULT 3
AAY77807
ID AAY7
XX AAY7
XX AAY7
XX Moti
XX Moti
XX Heli
XX Heli
XX Heli
XX Unic
XX Unic
XX Unic
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XX WO2C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The invention relates to a method of identifying a test composition that CC modulates the efficiency of translation termination comprising contacting the RNA helicase MTTI with a composition or agent under conditions CC permitting binding between the MTTI and the composition, detecting CC specific binding of the test composition or agent inhibits the MTTI. The CC composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the CC functional activity of mRNAs by altering frameshift frequency, permit CC transferase activity during initiation, promote degradation of aberrant CC transferase activity during initiation, elongation, termination and mRNA CC degradation of translation. The agents, which may be antagonists or conditions resulting from or cause premature translation, conditions resulting from or cause premature translation, conditions as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular CC Dystrophy, Haemophilia A, Haemophilia B, Von Willebrand Disease, CHischbercholesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis, content monitor and sequence of the yeast translation termination modulation content monitor of the yeast translation termination modulation.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY77807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein motif IV.
                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-globin; Duchene/Becker Muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Motif IV comprised in a gene modulating translation termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY77807 standard;
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                                                                                                                                                                                                                                                                                                                          22-JUL-1998;
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILAGDXXQLP
                                                                                                                                                                                                       Czaplinski
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                                                                                                                                                                                                                                                                                                                          98US-00120435
                                                                                                                                                                                                                                                                                                                                                                                   99WO-US016802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "reisdues indicated Xaa are unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                          Dinman
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dystrophy; antianemic.
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New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.

Claim 36; Page

79; 89pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                      21-FEB-2002; 2002US-0360039P
                                              20-FEB-2003; 2003US-00369493.
                                                                                              US2003233675-A1
                                                                                                                      Bacteria
                                                                                                                                                                                                                                          Bacterial polypeptide #10288.
                                                                                                                                                                                                                                                                  02-DEC-2004
                                                                                                                                                                                                                                                                                          ADS21255;
                                                                                                                                                                                                                                                                                                                ADS21255 standard; protein;
                                                                      18-DEC-2003
(CAOY/) CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                            polypeptide
                                                                                                                                                                                                                                                                  (first entry)
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100.0%; Pred. No. 0.:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                  611 AA
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0.15;
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CC comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC phosphorus use and/or uptake, by modification of protosynthesis or by providing improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress ccope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic companies from INSPPO at secretar inspire of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 10288; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-061375/06
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                                           segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to a recombinant DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  construct comprising
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Sequence 13

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used

for modulating translation termination

genes of

Length 13

mRNA at a nonsense codon and/or promote degradation of aberrant transcripts in cells. The method can be used to identify agents/compositions modulating binding to MTT1, useful to identify gene; sequences AAY/7804-812 represent motifs I-IX comprised in the general composition.

cc eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to complex can be definitely transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in cy pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or cy frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker CC muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding councied acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved in cy peptidyl transferase activity during translation, inhibiting the complex of interaction between MTT1 and eRF3 or involved in enhancing translation. Vectors comprising polymucleotides encoding the complex (or interfere with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They can be also useful to modulate activity during translation termination of mRNA and/or promote degradation of aberrant accompanies compositions useful as above, and/or used to complex as a nonsense codon and/or promote degradation of aberrant accompanies codon and/or promote degradation for translation of cells. They

carry out translation termination in eukaryotic cells, peptidyleukaryotic release factor (eRF) 1 and eRF3. The complex can be

Translation Termination) and the conserved proteins known to interact and

invention provides a new multiprotein complex which can modulate tidyl transferase activity during translation. The complex comprises gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of

밁 Ş Matches Query Match Sequence 611 AA; Local 376 w Similarity 8; Conserv ILAGDHLQLP 385 ILAGDXXQLP 12 Conservative 86.4%; <u>.</u>. Score 38; DB Pred. No. 10; Mismatches 8 '-2 Length 611, Indels 0, Gaps 0,

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RESULT 5
ADS430966
ID ADS4
XX ADS4
AC ADS4
AC ADS4
XX Bact
XX Recc
KW Recc
KW Coll
KW Datl
KW Bact
XX Bact
XX US21
                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                 Bacteria
                                                                                                                                                                                                                                                                               Bacterial polypeptide
                                                                                                                                                                                                                                                                                                                            02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       ADS43096;
                                                                                                                                                                                                                                                                                                                                                                                                               ADS43096 standard; protein; 642
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US2003233675-A1

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ADS42927
ID ADS4
XX ADS4
XX ADS4
XX DT 02-D
XX Bact
XX Recc
XW Recc
XW Cold
XW path
XW cold
XW homc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant cCC comprising the recombinant DNA construct and a method of producing a crop plant CCC transformed plant having an improved property. The plant is a crop plant CCC having an improved property comprises transformed plant with the CC polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the grope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic company form under a gradar under a serial patent and condition are condition. This sequence represents a bacterial polypeptide used in the grope of the invention are condition but was obtained in electronic condition.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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(SLAT/)
(CHEN/)
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                                                                                                                  Bacterial polypeptide #21357.
                                                                                                                                                          02-DEC-2004
                                                                                                                                                                                                ADS42927;
                                                                                                                                                                                                                                 ADS42927 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 642
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CHEN X.
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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant by a construct and a method of producing a crop plant CC such as maize or soybean. The method of producing a transformed plant CC thaving an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modificates better protein yield and/or CC content, improved yield by modification of carbohydrate, nitrogen or CC phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.
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Sequence 648 AA;
                                                                                              production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                  roduction. This sequence represents a bacterial polypeptide used in the cope of the invention. Note: The sequence data for this patent did not orm part of the printed specification but was obtained in electronic
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SLATER S
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                                      seqdata.uspto.gov/sequence.html
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RESULT: 7
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                         ADS41904;
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                                                                                                 ILAGDXXQLP 12
                                                                                 ILAGDHRQLP
                                                                                                                Conservative
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                                       protein; 648
                                                                                 407
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Pred. No.
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11;
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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC recombinant DNA construct and growing the transforming a plant with the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of protosynthesis or by providing improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. Note: The sequence data for this patent did not form part from its expresser as a betterial polypeptide used in the group of the invention. Note: The sequence data for this patent did not form part from its production and the printed specification but was obtained in electronic conditions.
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                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 20334; 122pp; English.
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HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                            Similarity
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ILAGDHKOLP 414
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                                                                                                                               Conservative
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RESULT 9
ADN18615
ID ADN1
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AC ADN1

ADN18615 standard; protein; 656

ADN18615;

RESULT 8

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Best Local S
                                                                    Matches
                                                                                                                                                                    polymerase chain reaction (PCR). Some of the proteins also stabilize duplaxes during polymerase reactions or improve exonuclease reactions, for example RFA also improves specificity of nucleic acid/protein interaction and PCNA improves polymerase-mediated repair processes and hybridization reactions. Nucleic acids encoding the archaeal polypeptides are used for recombinant production of proteins, and fragments of the nucleic acid as probes and primers for screening related sequences. The accessory proteins increase accuracy and efficiency of polymerase reactions, allow use of lower denaturation and extension temperatures (possibly isothermal processing), and improve synthesis of long targets. The present sequence represents a P. furiosus recombinant helicase dna2
                                                                                                                                                                                                                                                                                                                                                                  The invention provides a composition (A) for enhancing nucleic acid polymerase reactions that comprises an archaeal MCM (minichromosome maintenance.protein) and at least one of the archaeal polypeptides (PCNA, RFC-P38 or -P55, RFA, CDC6, FEN-1, dUTPase, ligase, helicase dna2, or helicases 2-8). (A) And similar compositions containing different combinations of accessory proteins, are used to improve performance of synthesis, amplification, mutagenizing, labeling and detecting reactions, e.g. for gene characterization, cloning, detection of allelic variants, e.g. for gene characterization, cloning, detection of allelic variants, and screening for disease, particularly where done by
                                                                                                                                      Sequence 655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCM; minichromosome maintenance protein; archaeal polypeptide; PCNA; RFC-P38; RFC-P55; RFA; CDC6; FEN-1; dUTPase; ligase; helicase dna2; PCR; nucleic acid amplification; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 182; Fig 35; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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DB; AAF57035.
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02-DEC-2004

(first entry)

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CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC having an improved property comprises transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plants with CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress CC condition, This sequence represents a bacterial polypeptide used in the growth from untered specification but was obtained in electronic forms part of the printed specification but was obtained in electronic component from under the grades under the servers under the servers conficient on the sequence represents and conficient on the sequence conficient on the sequenc
                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
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                                                                                                                                                                                                                                                                                              Sequence 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1268; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAOY/)
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                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a robial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲
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HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                             from USPTO
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                                                                                                                                                                                    Similarity
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ILAGDHKQLP
                                                                          ILAGDXXQLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorus; photosynthesis; lignin; galactomannan;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide #1268
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414
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                                                                                                                                                                                86.4%;
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                                                                                                                                                 0;
                                                                                                                                                 Score 38; DB Pred. No. 11; 0; Mismatches
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Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;

eRF3;

0

helicase; Dipl.

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RESULT 10
AAO26745
ID AAO26745
AC AAO26
RESULT 11
AAY77816
ID AAY77
XX AAY77
XX AAY77
XX 31-MA
DT 31-MA
XX Yeast
XX Helic
KW Helic
KW beta-
KW helic
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid encoding a tannic acid responsive element-coupling protein. The transcription controller is useful in an antiretrovirus agent and nerve growth/maintenance controlling agent for growth inhibition of a retrovirus. The protein can be used for developing a new low molecular compound controlling transcription control. This sequence represents a rat protein sequence relating to the transcription controller of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 988
                                                                                                                                Yeast Dip1
                                                                                                                                                                                    31-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                         AAY77816 standard; peptide; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a transcription controller comprising a nucleic acid encoding a tannic acid responsive element-coupling protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 2; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 element-coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A transcription controller, useful for inhibiting the growth of a retrovirus, comprises a sequence encoding a tannic acid responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TANU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001; 2001JP-00065803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiviral; gene therapy; transcription controller; antiretrovirus agent; tannic acid responsive element-coupling protein; nerve growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 988-mer rat
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SUMITOMO
ZH HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                               ILAGDHRQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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RESULT 12
ABW01204
ID ABW01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferase activity, especially diseases resulting from a nonsense or compared from the component of the complex of the compl
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 414
                           15-JAN-2004
                                                                           ABW01204;
                                                                                                                      ABW01204 standard; protein; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group I helicases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Translation Termination) and the conserved proteins known to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-171458/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1998;
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                                                                                                                                                                                                                                                                                          3 ILAGDXXQLP 12
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                                                                                                                                                                                                                                                                                                                                          Similarity 70.
                                                                                                                                                                                                                                               VLAGDNKQLP 202
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                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provides a new multiprotein complex which can modulate
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                                                                                                                                                                                                                                                                                                                                        ; Score 37; DB
; Pred. No. 11;
1; Mismatches
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                                                                                      Query Match
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Matches 7
                                                                                                                            The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations.
                                                                                    Sequence 414 AA;
                                                                                                                                                                                                                                                                        Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                                                                                                                                                                                                                                                                                 WPI; 2003-810549/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae DIP1 protein
                                                                                                                The present sequence is Saccharomyces cerevisiae
                                                                                                                                                                                                                              Disclosure; Col 55-58; Opp; English.
                                                                                                                                                                                                                                                         binding to Mttl.
                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                           (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
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                            7; Conserv
  ILAGDXXQLP 12
                                                                                                                                                                                                                                                                                                                                                           Czaplinski K,
                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9905-00359268
                                           84.1%;
                                                                                                                                                                                                                                                                                                                                                              Dinman
                                            Score 37; DB Pred. No. 11;
                               Mismatches
                                                           7;
                               2
                                                           Length 414;
                                                                                                                DIP1 protein
                                Indels
                               0
                                Gaps
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ADP44130
ID ADP44
XX ADP44
XX ADP44
XX IB-NC
XX Yeast
XX Heame
XW Pepti
XW Pepti
XW Neuro
XX 17-Ju
XX 28-Au
                                                                                                                                                                                                     frameshift frequency; abbrrant transcript degradation; petetidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; Haemophilia B; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Cystic fibrosis; Ovarian Cancer; Wilms Tumour; Hirschapprung disease; Cystic fibrosis; Kidney Stone; Pamilial hypercholesterolaemia; Retinitis Bigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast; enz)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast helicase Dipl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP44130 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLAGDNKOLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                yeast; enzyme
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28-AUG-2003; 2003US-00652334.

US2004115787-A1

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying a test composition that CC modulates the efficiency of translation termination comprising contacting the RNA helicase MTT1 with a composition or agent under conditions compering contacting the RNA helicase MTT1 with a composition or agent under conditions of permitting binding between the MTT1 and the composition, detecting composition and methods are useful for modulating the fidelity of composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the composition and methods are useful for modulating the fidelity of functional activity of mRNAs by altering frameshift frequency, permit composition and provide modulators (inhibitors/stimulators) of permit composition of aberrant composition of a termination event, promote degradation of aberrant composition, and provide modulators (inhibitors/stimulators) of peptidyl transferase activity during initiation, elongation, termination and mRNA composits, are useful in screening, diagnostic and therapeutic purposes, correlation, as beta-thalassasemia, beta-globin, Duchenne/Becker Muscular corresponding and the seases, continuation, promote degradation of translation, promote degradation of translation, constant cancer, Ovarian Cancer, Wilms Tumour, constant disease, continuation, and the sequence represents continuations, and present sequence represents continuations, and sequence represents continuations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent inhibits the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1998;
22-JUL-1999;
                                                   bacterial
                                                                   nitrogen;
                                                                                    pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carb
                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
                                                                                                                                                                                               Bacterial polypeptide #2884.
                                                                                                                                                                                                                                       02-DEC-2004
                                                                                                                                                                                                                                                                          ADN20231
                                                                                                                                                                                                                                                                                                          ADN20231 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 28; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DINM/) DINMAN J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                      193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      VLAGDNKQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                           ILAGDXXQLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence of the yeast helicase Dipl.
                                                 phosphorus; photosynthesis;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
                                                                                                                                                                                                                                     (first entry)
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99US-00359268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.1%;
70.0%;
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                                                                                                                                                                                                                                                                                                              650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB Pred. No. 11; 1; Mismatches
                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                    lignin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 414;
                                                                                        yield; carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Bacteria

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance;

Bacterial polypeptide #21645.

(first

entry)

0,

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ADS43215
ID ADS43
XX ADS43
AC ADS43
XX D2-DE
XX D2-DE
XX Recom
KW Cold
KW patho
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                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC comprising the recombinant DNA construct and a method of producing a crop plant (CC transformed plant having an improved property. The plant is a crop plant (CC transformed plant having an improved property. The plant is a crop plant (CC such as maize or soybean. The method of producing a transformed plant (CC having an improved property comprises transforming a plant with the (CC recombinant DNA construct and growing the transformed plant, where the (CC polynucleotide or polypeptide is useful for improving plant properties. (CC improved plant properties, e.g. improved cold, heat or drought tolerance, (CC improved plant properties, e.g. improved cold, heat or drought tolerance, (CC increased resistance to plant disease, better growth rate by modification (CC increased resistance to plant disease, better growth rate by modification (CC increased resistance to plant disease, better growth rate by modification (CC increased resistance) (CC increased recombination, modification of carbohydrate, nitrogen or (CC increased rate of (CC increased rate of (CC increased rate)) (CC increased rate) (CC 
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter functional in a plant cell, where the promoter is positioned provide for expression of a polynucleotide encoding a polypeptide from microbial source. The invention also relates to a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                    ADS43215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             format from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GOLD/)
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                                                                                                                                                                                                                                                                                                                             404
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SLATER S
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOLDMAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEN
                                                                                                                                                                                                                                                                                                                                                                        ILAGDXXQLP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2884; 122pp; English.
                                                                                                                                                                                                                                                                                                                             VLAGDHKQLP 413
                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at
                                                                                                                                                                                                                  protein; 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                    84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to a recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Search completed: April 18, 2005, 08:03:46
Job time : 61.8483 secs
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                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAOY/)
(HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
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                                                                                                                                                                                                                      Sequence 653 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 21645; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOLDMAN B S.
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                                                                       VLAGDHKQLP
                                                                                                               ILAGDXXQLP 12
                                                                                                                                                   Conservative
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                                                                                                                                                                  84.1%;
                                                                                                                                               Pred. No. 19;
1; Mismatches
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                                                                                                                                                                                      8; Length 653;
                                                                                                                                                   Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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   79.5
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US-09-359-268A-4
US-09-359-268A-20
US-09-359-268A-20
US-09-359-268A-20
US-09-248-796A-15170
US-09-248-796A-1570
US-09-252-991A-17570
US-09-252-991A-17570
US-09-270-767-42726
US-09-270-767-42726
US-09-270-767-42726
US-09-28-335-6
US-09-28-335-801
US-09-38-352-6205
US-09-18-352-6205
US-09-18-352-6205
US-09-18-352-6205
US-09-18-352-6205
US-09-359-268A-27
US-09-359-268A-27
US-09-425-335-2
US-09-425-335-2
US-09-426-395-2
US-09-306-396-6
US-09-306-398-6
US-09-489-039A-12239
US-09-540-236-3464
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1517, Ap
1517, Ap
17570, A
17570, A
4679, Ap
58044, A
42726, A
42726, A
42726, A
58044, A
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28, Appl
1483, App
15170, A
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   3, Appli
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24, Appl
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24, Appl
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12278, A
12939, A
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29	29	29	29	29	30	30	30	30	30	30	30	30	30	32	31	31	31
65.9	65.9	65.9	S	65.9	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	68.2	70.5	70.5	70.5	70.5
218	165	165	154	118	857	770	648	556	539	514	422	407	202	856	788	508	472
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US-10-026-045-2	US-09-270-767-52991	US-09-270-767-37774	US-09-270-767-59910	US-09-949-016-7744	US-09-425-335-4	US-09-489-039A-7872	US-09-902-540-13835	US-09-425-335-7	US-09-134-000C-4363	US-09-489-039A-10028	US-09-248-796A-16512	US-09-634-238-240	US-09-252-991A-22316	US-09-107-433-3534	US-09-583-110-3939	US-09-252-991A-32269	US-09-359-268A-26
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
 Appli 	52991, A	37774, A	59910, A	7744, Ap	\mathbf{z}	7872, Ap	13835, A	7, Appli	4363, Ap	10028, A	16512, A	240, App	22316, A		3939, Ap	32269, A	26, Appr

ALIGNMENTS

RESULT 1 US-09-359-268A-4

US/09359268A

GENERAL INFORMATION: Sequence 4, Application Patent No. 6630294

A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES

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RESULT 2
US-09-538-092-1100
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APPLICANT: Czapliński, Kevin
APPLICANT: Czapliński, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPAMILY OF RNA HELIC
TITLE OF INVENTION: THE FIDELITY OF TRANSLAI
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
Sequence 1100, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERBNCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PRILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01
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SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
PEATURE:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 199-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
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US-09-538-092-483
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, NAME/KEY: misc_feature
; LOCATION: (0)....(0)
; OTHER INFORMATION: Polypeptide Accession Number P38935
US-09-538-092-1100
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SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1100
LENGTH: 993
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                            SEQ ID NO 483
                                                     APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
PILE REPERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
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APPLICANT:
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ORGANISM: Homo sapiens
LENGTH: 683
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Similarity 70.0%;
7; Conservation
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Similarity 80.0%;
8; Conservative
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THE FIDELITY OF TRANSLATION TERMINATION AND USES
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Pred. No.
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                                                                                                                             US-09-328-352-6971
                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-328-352-6971
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                                                                                                                                                                         APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6971
LENGTH: 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 15170
LENGTH: 426
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                        Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Sequence 6971,
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                               ORGANISM: Acinetobacter baumannii
                                                                                                                                                              TYPE: PRT
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140
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                              3 ILAGDXXQLP 12
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7; Conserv
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6562958
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Similarity 60.0%;
6; Conservative
                                                              Similarity 7; Conserv
IVAGDEFQLP 149
                                                                Conservative
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                                                                             79.5%;
70.0%;
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                                                                1; Mismatches
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Pred. No.
                                                                               Score 35; DB
Pred. No. 11;
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Pred. No. 7.8;
2; Mismatches
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RESULT 9
US-09-107-532A-4679
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                                   Sequence 4679, Application US/09107532A
PATENT NO. 6583275
PATENT INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                    Query Match 77.3%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13564
LENGTH: 513
TYPE: PRT
ORGANISM: Myxococcus xanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13564, Application US/09902540 Patent No. 6833447
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
CITEREPERENCE: 38-10 (1.5849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILB REFERENCE: 107196.136
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NUMBER OF SEQUENCES:
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Pred. No.
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                   and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-270-767-58044
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                                                                                                                   Sequence 58044, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,787
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 58044
LENGTH: 102
TYPE: PRT
Query Match 75.0%; Score 33; DB 4; Length 102; Best Local Similarity 60.0%; Pred. No. 4.5; Matches 6; Conservative 1; Mismatches 3; Indel8
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Best Local
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4679:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/051571
PILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (B) LOCATION 1...879 SEQUENCE DESCRIPTION: SEQ ID NO: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
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70.0%;
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US-09-425-335-6
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US-09-270-767-42726
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEINMANN, ROBERTO
TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF
FILE REFERENCE: db7 sequence
CURRENT APPLICATION NUMBER: US/09/425,335
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09425335
Patent No. 6518052
GENERAL INFORMATION:
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             SEQ ID NO 6
                                                                                                                            GENERAL INFORMATION:
APPLICANT: WEINMANN, ROBERTO
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Best Local Similarity
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LENGTH: 152
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Patent No. 6518052
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-09-270-767-42726
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                                        TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF FILE REFERENCE: db7 sequence
CURRENT APPLICATION NUMBER: US/09/425,335
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
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TYPE: PRT
ORGANISM: Yeast homolog
LENGTH: 805
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Pred. No. 40;
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US-09-328-352-6205
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US-09-248-796A-20596
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GATY L. BYETON et al.
APPLICANT: GATY L. BYETON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
PILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6205
LENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20596
LENGTH: 282
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PELLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
                                                                              Query Match
Best Local
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Patent No. 6562958
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ORGANISM: Candida albicans
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220 LSGDALQLP 228
                                4 LAGDXXQLP
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5; Conserv
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Pred. No.
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Pred. No. 24;
                                                                              Score 32; DB
Pred. No. 24;
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                                                                 Indels
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Search completed: April 18, Job time : 15.9781 secs

2005, 08:18:34

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
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11:
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10T_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10T_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10T_NEW_PUB.pep:*
cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
                                                                                                                                                                                                                                                                                  gm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
gm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
gm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
gm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
gm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
gm2_6/ptodata/1/pubpaa/PCSUS_PUBCOMB.pep:*
gm2_6/ptodata/1/pubpaa/PCSUS_PUBCOMB.pep:*
gm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
gm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 9 8 8 7 6 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
33333333333333333333333333333333333333	Score
00000000000000000000000000000000000000	Query Match Length
12 332 610 640 642 642 655 655	Length
166	DB
US-10-652-334-4 US-10-425-114-38637 US-10-425-114-37833 US-10-369-493-10288 US-10-424-599-233501 US-10-425-114-37717 US-10-369-493-1526 US-10-369-493-21357 US-10-369-493-21357 US-10-369-493-21357 US-10-369-493-21368 US-10-369-493-1268 US-10-369-493-1268	ID
Sequence 4, Appli Sequence 38637, A Sequence 37833, A Sequence 10288, A Sequence 233501, Sequence 37717, A Sequence 21526, A Sequence 21557, A Sequence 20334, A Sequence 20334, A Sequence 2034, Appli Sequence 208, Appli Sequence 28, Appli	Description

	.0 1076 10 US-09-935	75.	33	<u>.</u> 5
	.0 1024 15 US-10-369-493-34	75	u سا	4
	.0 828 15 US-10-144-19	75.	ω W	43
	.0 821 15 US-10-369-4	75.	ω u	42
	.0 819 15 US-10-369-	75.	ω G	41
	.0 817 15 US-10-282-122A-7473	75.	33	40
	.0 798 15 US-10-282-	75.	33	39
	.0 787 15 US-10-282-122A-7246	75.	33	38
7	.0 744 15 US-10-282-122A-551	75.	33	37
	.0 723 15 US-10-369-	75.	ω u	36
	.0 677 16 US-10-	75.	33	35
u	.0 592 15 US-10-282-122A-6505		33	34
5	.0 581 15 US-10-282-122A-6590	•	33	33
	.0 562 15 US-10-104-	•	33	32
ö	.0 472 15 US-10-282-1	•	33	31
34	.0 416 15 US-10-424-	75.	33	30
7	.0 312 15 US-10-425-114-4579	75.	33	29
2	.0 309 15 US-10-425-114-3905	75.	33	28
10	.0 133 15 US-10-424	75.	33	27
77	.3 862 15 US-10-282-122A-57	77.	34	26
	.3 693 15 US-10-		34	25
	.3 640 15 US-10-26	77.	34	24
	.3 608 15 US-10-262	77.	34	23
	.3 10 10 US-09-572	77.	34	22
5	.5 739 15 US-10-282	79.	35	21
	.5 640 17 US-10-926-543	79.	35	გ 0
•	.8 663	81.	36	19
	.1 830 15 US-10-	84.	37	18
	.1 683 15 US-10-369-493-2226	٠.	37	17
	.1 653 15 US-10-369-493	84.	37	16
	.1 650 15 US-10-369-493-	84.	37	15
N	.1 626 16 US-10-437-963-166322	84.	37	14

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/652,334;
CURRENT FILING DATE: 2003-08-28;
PRIOR APPLICATION NUMBER: US/09/359,268A;
PRIOR FILING DATE: 1999-07-22;
PRIOR APPLICATION NUMBER: 60/093,685;
PRIOR FILING DATE: 1998-07-22;
NUMBER OF SEQ ID NOS: 32;
SOFTWARE: PATENTIN Ver. 2.0;
SEQ ID NO 4
문
                                     S
                                                                                                                                                                            US-10-652-334-4
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US-10-652-334-4
                                                                                    Best Loc
Matches
                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPLANILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                             LENGTH: 12
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
PRATURE:
PRATURE:
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 601-1-85N
                                                                                                      Local
                                       w
                                                                                    l Similarity
10; Conserv
                                       ILAGDXXQLP 12
ILAGDXXQLP 12
                                                                                 86.4%; Score 38; DB 16; Length 12; llarity 100.0%; Pred. No. 0.15; Conservative 0; Mismatches 0; Indels
                                                                                    0
                                                                                    Gaps
                                                                                      0
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53313)B; CURRENT FILING BATE: 2003-04-28; NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37833
LENGTH: 404
TYPE: PRT
RESULT 4
US-10-369-493-10288
; Sequence 10288, Application US/10369493
; Publication No. US20030233675A1
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US-10-425-114-38637
                                                                                                                                                                                                                              US-10-425-114-37833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38637
LENGTH: 332
                                                                                                                                                                 Matches
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37833, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38637, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                             ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: 700618821_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                              Y Match 86.4%;
Local Similarity 80.0%;
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                                                                                                    ILAGDHLQLP 163
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Kovalic, David K.
Screen, Steven E
                                                                                                                                                                 Conservative
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                                                                                                                                                                              Score 38; DB 15;
Pred. No. 6.2;
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Pred. No.
                                                                                                                                                               Mismatches
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                                                                                                                                                                                              Length 404;
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53223)B; CURRENT APPLICATION UNMBER: US/10/424,599; CURRENT FILING DATE: 2003-04-28; NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 233501
LENGTH: 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLATIFLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-29
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                         RESULT 6
US-10-425-114-37717
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                                                                                                                                                                                                                                                                                                                                       US-10-424-599-233501
Sequence 37717, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
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LENGTH: 611
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Best Local Similarity
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APPLICANT: Hink
APPLICANT: Slat
APPLICANT: Gold
APPLICANT: Chen
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                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(637)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_52878C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 ILAGDHLQLP 385
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80.0%;
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Pred. No. 9.
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US-10-369-493-21526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3170-056-H12_FLI.pep
US-10-425-114-37717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Methanobacterium thermoautotrophicum US-10-369-493-21526
                                                                                                                                                                                                                                             US-10-425-114-37557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21526
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILB REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37717
LENGTH: 639
TYPE: PRT
ORGANISM: 639
CORGANISM: Glycine max
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OP INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REFERENCE: 38-10 (52052) B
CURRENT PEPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                              APPLICANT:
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILS REFERENCE: 38-21(53313)B
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                                                                                                                                                                                                                                                                                                                       390 ILAGDHRQLP 399
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Similarity 80.0%;
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                                                           Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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Pred. No.
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Pred. No. 10;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20334
LENGTH: 648
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37557
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Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
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8; Conserv
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8; Conserv
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Pred. No.
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; TYPE: PRT
; ORGANISM: Archaeoglobus
US-10-369-493-21357
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TYPE: PRT
; ORGANISM: Pyrococcus horikoshii
US-10-369-493-1268
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US-10-369-493-1268
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CURRENT APPLICATION NUMBER: 024/10/828,924
CURRENT FILING DATE: 2004-04-20
PRIOR APPLICATION NUMBER: 60/146,580
PRIOR APPLICATION NUMBER: 60/146,580
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
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                                   Matches
                                                                Query Match
                                                                                                                                                                           SEQ ID NO 1268
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Publication No. US20030233675A1
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Publication No. US20050003401A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Canada Color Chen
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-26
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 80.0%;
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3 ILAGDXXQLP 12
                               Similarity 80.0
8; Conservative
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                                                   86.4%;
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Pred. No.
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Pred. No.
                                   Mismatches
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                                                                                   US-10-437-963-166322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: P
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 166322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166322, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Peltz,
APPLICANT: Czapl
APPLICANT: Dinma
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 38-21(53221)8
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                                                                                                     FEATURE:
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NAME/KEY: unsure
LOCATION: (1)..(626)
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                                                                                                                                                                                                    ORGANISM: Oryza sativa
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Boukharov, Andrey A.
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ALIGNMENTS

submitted to the EMBL Data Library, September 1998
A; Description: Arabidopsis thaliana chromosome II BAC T18R17 ---A; Accession: T02699
A; Status: ***--* RESULT 2 D69085 probable helicase At2903270 [imported] - Arabidopsis thaliana NyAlternate names: hypothetical protein T18812.6 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_chan. C;Accession: T02699; D84446 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84446 A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, I
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999 밁 S A; Map position: 2 C; Superfamily: probable DNA helicase MJ0104 A; Gene: At2g03270; T18E12.6 A; Molecule type: DNA A; Residues: 1-635 < STO> A; Status: preliminary A;Cross-references: UNIPROT:O81047; EMBL:AC005313; NID:g3548797; PID:g3548803 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-635 <ROU> T02699 RESULT 1 Cross-references: GB:AE002093; NID:g4335770; Matches Best Local Query Match 386 3 ILAGDXXQLP 12 Similarity 8; Conserv |||| ||| Conservative 395 86.4%; Score 38; Pred. No. Mismatches DB 1.5; PIDN: AAD17447.1; GSPDB:GN00139 2 Length 635 M.I.; Town, C.D.; Fujii, C.Y.; <u>;</u> Gaps L.; Tallon, L 0 Ron

transcription control factor enhancer-binding protein - Methanobacterium thermoautotroph C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: D69085 C;Accession: D69085 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. riol. 179, 7135-7155, 1997

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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sek: M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogucl DNA Res. 5, 55-76, 1998
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                            probable DNA-binding protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: E71080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69423
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                                                                                        A;Cross-references: UNIPROT:O58624; GB:AP000004; NID:g3236131; PIDN:BAA30003.1;
                                                                                                                    A;Residues: 1-656 <KAW>
                                                                                                                                     A; Molecule type: DNA
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C;Superfamily: probable DNA helicase MJ0104
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;Species: Archaeoglobus fulgidus
;Jate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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0; Mismatches
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                                            interim accession
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Query Match

98 .48;

Score

38; DB

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Length

656;

Local

Similarity

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A; Note: RIP1
C; Complex: ri
C; Function:
                                                             A;Cross-references: GDB:434023; OMIM:600502
A;Map position: 11q13.2-11q13.4
C;Keywords: immunoglobulin; single-stranded
                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 'GGRV', 495-862,'K', 864-865,'T' <
A; Cross-references: GB: M64979; NID: g183249;
A; Experimental source: brain stem
                                                                                                                                                                                                                                                                         J. Biol. Chem. 266, 15876-15881, 1991
A;Tittle: A recombinant cDNA derived from human brain encodes a DNA binding protein A;Reference number: A40804; MUID:91340730; PMID:1714899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 02-Ju
C;Accession:
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P38935; GB:L14754
R;Kerr, D.; Khallli, K.
J. Biol. Chem. 266, 15876-15881, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change
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J. Biol. Chem. 270, 21503-21508, 1995
A;Title: Molecular characterization of the rat insulin enhancer-binding
A;Reference number: Z24545; MUID:95394901; PMID:7665561
A;Accession: T48845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mesocricetus auratus (golder
C;Date: 02-Jun-2000 #sequence_revision
C;Accession: T48845
                                                                                                                             A;Gene: GDB:IGHMBP2
                                                                                                                                                                       A; Note: the authors translated the codon CAG for
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-993 < FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Pukita, Y.; Mizuta, T.R.; Shirozu, M.; Ozawa, K.; Shimizu, A

D. Biol. Chem. 268, 17463-17470, 1993

A;Title: The human Smubp-2, a DNA-binding protein specific to

A;Reference number: A47500; MUID:93352537; PMID:8349627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig mu chain switch region binding protein 2 - human
N;Alternate names: DNA-binding protein S-mu-bp-2; glial factor 1; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: the 3b2 complex is one ent RIPE3a [validated, MUID:95394901]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q60560; EMBL:L15625; NID:g290918; PIDN:AAB00104.1; PID:g2909:
A;Experimental source: tissue type insulinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-989 <SHI>
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                                                           immunoglobulin; single-stranded DNA binding
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Score 38;
Pred. No.
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Pred. No.
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  DB 2.4;
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                              probable DNA helicas PAB1561 - Pyrococcus abyssi (strain Orsay) C,Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
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A;Accession: G72429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi. Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A;Title: Isolation of cDNA encoding a binding protein specific A;Reference number: S35633; MUID:93261806; PMID:8493094
A;Accession: S35633
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A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-650 <ARN>
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A;Residues: 1-993 <MIZ>
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;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: probable DNA helicase MJ0104
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                      ;Genetice:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA binding
                                                                                                                                                                                                                                                                                         h 84.1%; Score 37; DB Similarity 70.0%; Pred. No. 2.6 7; Conservative 1; Mismatches
                                                                    B75105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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6;
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                                                                                  #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                             Length 650;
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           RESULT 11
C84367
DNA binding protein eukaryotic-like
C;Species: Halobacterium sp. NRC-1
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R;Rieger, M.
submitted to the Protein Sequence Database,
A;Reference number: S37832
A;Accession: S37834
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S34700
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P34243; EMBL:X74152; NID:g450363; PID:g395256
A;Experimental source: strain S288C
R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C. submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: Sequencing and analysis of 51.5 kilobases A;Reference number: S34679
A;Accession: S34700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G;Species: Saccharomyces cerevisiae
G;Species: Saccharomyces cerevisiae
G;Date: 31-Dec-1993 #text_change 09-Jul-2004
G;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
G;Accession: S34700; S37830; S37834
R;Wieman, S:; Voss, H.; Schwagaer, C:; Rupp, T.; Stegemann, J.; Zimmermann, submitted to the EMBL Data Library, July 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A;Molecule type: DNA
A;Residues: 1-653 <KAM>
A;Cross-references: UNIPROT:Q9UZB6; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5014
                                   8
                                                                                                                                                                                                                                                    A;Cross-references: SGD:S0001500; MIPS:YKL017c
A;Map position: 11L
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z28017; NID:g486006; PID:g486007; MIPS:YKL017c A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-683 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z28017; NID:g486006; PID:g486007; A;Experimental source: strain S288C
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A; Residues: 1-683 <WI2>
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A; Residues: 1-683 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable purine nucleotide-binding protein YKL017c - yeast (Saccharomyces cerevisiae)
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A; Accession: B75105
                                                                                                                                                                                                                                                                                                   A;Gene: SGD:DIP1
                                                                                   Best Loc
Matches
                                                                                                                                                                                        Superfamily: probable DNA helicase MJ0104;
Keywords: ATP; P-loop; purine nucleotide binding;
229-236/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                      235/Binding
                                                                                                                           Query Match
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7; Conserva
                                                                                                       Similarity
VLAGDNKQLP
                                          ILAGDXXQLP 12
                                                                                                                                                                      site: ATP/GTP (Lys)
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                                                                                   Conservative
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429
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70.0%;
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Pred. No. 2.6;
                                                                                                       Score 37; DB 2; Pred. No. 2.7;
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                                                                                                                         Length 683;
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[imported]

Halobacterium

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R.Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blai; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannass A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Max Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950 A; Accession: C84367
                                                                                                                                                                                                                                                                                                                                     H64312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70476
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C;Accession: C84367
  A; Cross-references:
                                                                                A; Reference number: A64300;
A; Accession: H64312
                                                                                                                                                                                                                                                                      C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                  probable DNA helicase MJ0104 - Methanococcus jannaschii
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A; Residues: 1-751 <STO>
                                         A; Molecule type: DNA
                                                           A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-530 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                          283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501
                        1-663 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
Similarity 70.0%;
7; Conservation
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  UNIPROT:Q57568; GB:U67467;
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Pred. No. 3
1; Mismatch
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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                                                               not shown; translation
GB:L77117; NID:g2826242; PIDN:AAB98084.1;
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D.W.; Maddocks, D.(
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conserved hypothetical protein HP0447 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Species: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: G64575

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D., Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Accession: G64575

A;Accession: G64575
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G64575
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A;Map position: FOR99243-101234
A;Start codon: TTG
C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-774 <STO>
A; Cross-references: UNIPROT: Q9HYB8;
A; Experimental source: strain PAO1
C; Genetics:
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable ferredoxin PA3491 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #semianos ~~~**-*-
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C;Superfamily:
                                                                                                             A;Residues: 1-360 <TOM>
A;Cross-references: UNIPROT:025195;
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
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A; Reference number: A82950;
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R;Stover, C.I
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Pred. No.
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Search completed: April 18, 2005, 08:06:01 Job time: 12.562 secs

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Q7S1L9
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Ē	Q09594	Q8g3n4	Q86u01	025195	Q6n3j4	Q8eav3	Q9hyb8	Q8rce3	Q6bk27	Q75cl7	Q8bh04	Q6fae6	Q9q8k3	Q75ja0
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ALIGNMENTS

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RESULT
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ID Q7
AC Q7
D7 05
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Q72RC7;
Q5-JUL-2004
05-JUL-2004
05-JUL-2004
                                 Hypothetical protein.
OrderedLocusNames=LIC11819;
Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
EMBL; AE017176; AA066376.1; -.
TIGR; PG1303; ...
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Nelson K.B., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M. Haft D.H., Kolonsy J.F., Nelson W.C., Mason T.M., Tallon L., G Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.B., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004386; P:helicase activity; IEA.
Complete proteome; Helicase.
SEQUENCE 471 AA; 52502 MW; FA887E18B8
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OrderediocusNames=PG1303;
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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NCBI_TaxID=44275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILAGDMAOLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILAGDXXQLP 12
                                                                                                                                                                                                                                    (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Last annotation update)
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Pred. No. 2.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                         Leptospira
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QBF4E3
1D QBF4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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D. Bacteriol. 186:2164-2172 (2004).
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Best Local
                           EMBL; AE011381; AAN49297.1; -.

GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004003; F:ATP-dependent DNA heli
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003666; F:DNA cepair; IEA.
GO; GO:0000166; F:DNA repair; IEA.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR011545; UYDD-helicase.
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Q8F4E3;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai; MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597; Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H., Zeng Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Saint Girons I., Somerville R.L., Wen Xu J.-G., Zhao G.-P.; Xu Juger Physiological and pathogenic interrogans revealed by whole-genome Nature 422:888-893(2003).
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SEQUENCE FROM N.A.
STRAIN=Fiocruz L1-130;
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000166; F:nucleotide binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=LA2098;
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01-MAR-2004
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ATP-binding; Complete p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA ATPase.
InterPro; IPR000212; UvrD-helicase.
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8; Conserv
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3 (TrEMBLrel. 23,
4 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 AA;
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Pred. No. 6.3;
D; Mismatches
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8C62B954412AF267 CRC64;
                                                                                                                                                                                                                                                                                                           DNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   features of Leptospira
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                                                                                                                                                                                                                                                                                                               activity; IEA
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RESULT
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Q9FNX9
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Best Local Similarity
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Best Local (
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                                                                                                                                                      081047; Q94AT0;
081047; Q94AT0;
01-NOV-1998 (TERMELrel. 08
01-UN-2002 (TERMELrel. 21
05-UN-2004 (TERMELrel. 27
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SMART; SM00487; DEXDC; 1.
ATP-binding; Complete proteome.
SEQUENCE 634 AA; 72600 MW;
              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                               Putative helicase. Name=At2g03270;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Whole plant;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  photosynthesis gene promoter.";
J. Biol. Chem. 10:1074-1074(2001).
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NCBI TaxID=3702;
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35 AA; 70335 MW; 6149646686631F29 CRC64;
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Pred. No. 6.3;
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A Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
A Bavis R.W., Ecker J.R., Theologis A.;
Bubmitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006284; AAD17447.2; -.
BR EMBL; AV045820; AAK15033.1; -.
BR EMBL; AV045820; AAK15033.1; -.
BR EMBL; AV091361; AAM14300.1; -.
BR EMBL; AV091361; AAM14300.1; -.
BR ENBL; T02699, T02699.
                                                                                                                                                                                                                 Matches
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Best Local (
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InterPro; IPR001545; DRAD\(DRAH N.)
InterPro; IPR004488; Dut_DNA_helic.
SMART; SM00382; AAA; 1.
SMART; SM00387; DEXDC; 1.
TIGRPAMB; TIGR00376; Dut_DNA_helic; 1.
ATP-binding; Helicabe.
SEQUENCE 639 AA; 70850 MW; C91340DAE
027671 PRELIMINARY;
027671;
01-JAN-1998 (TREMBLIEL 05,
01-JAN-1998 (TREMBLIEL 05,
01-MAR-2004 (TREMBLIEL 26,
Transcriptional control fact
OrderedLocusNames=MTH1634;
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
Lin X., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Liu S.X., Sakano H., Pham P.K.,
Goldsmith A.D., Lee J.M., Quach H.L., Tori
Carninci P., Chen H., Cheuk R., Hayashizak
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Barnstead M.B., Mason T.M., Bowman C.L., Town Cning
Carrera A.J., Creasy T.H., Buell C.R., Town C.D.,
Fraser C.M., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                      GO:0005524; F:ATP binding; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0004386; F:helicase activity; I
GO:0000166; F:nucleotide binding;
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y S.D., Lin X., Ka
, Ronning C.M., F1
ed (MAR-2000) to t
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tor (Enhancer-binding protein)
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Pred. No. 6.3;
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                                                                                      PRT;
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.M., Somerville C.
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C.M., Benito M.-I.,
, Nierman W.C.,
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O28883; O1-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-MAR-2004 (TrEMBLrel. 26, L
reducing archaeon Archaeoglobus fulgidus.";

EMBL, AE001009; AAB89860.1; -.

PIR; C69423; C69423.
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STRAIN-VC-16 / DSM 4304 / DSM 4305 DOI=10.1038/37052;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,

Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,

Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,

Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,

Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,

Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith D.R., Doucette-Stamm I.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Wierzboweki J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzboweki J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietroveki S., Church G.M., Daniels C.J., Mao J.-I., Rice of Mechanobacterium thermoautotrophicum "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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OrderedLocusNames=AF1388;
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GO; GO:0005524; F.ATP binding; IRA.
GO; GO:0003677; F.DNA binding; IRA.
GO; GO:0000166; F.nucleotide binding;
InterPro; IPR003593; AAA ATPase.
InterPro; IPR004483; put_DNA_helic.
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STRAIN=VC-16 / DSM
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 6.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278DA65037229377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648
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6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT
OS 6624
ID 624
ID 625
DT 05
DT 011
DT 011
DT 01
DT 02
OS Py
OS PY
OX NC
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Best Local
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Best Local :
                                                                                                                                                                                                                                                                                                O58624 PRELIMINARY; PRT; 656 AA.
O58624;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
656aa long hypothetical DNA-binding protein.
OrderedLocusNames=PH0909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R. B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; ABC10180; AAL80696.1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

SMART; SM00487; DEXDC; 1.

TIGRPAMS; TIGR00376; put_DNA_helic; 1.

Complete proteome.

SEQUENCE 655 AA; 74581 MM; 0AB579DA14A8EBDO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8U398
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004386; F:helicase activity; IEA.
GO; GO:0000166; F:nuclectide binding; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003483; put_DNA_helic.
SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR00376; put_DNA_helic; 1.
ATP-binding; Complete proceome; Helicase.
ATP-binding; Complete proceome; Helicase.
SEQUENCE 648 AA; 73775 MW; B5074507D856A7D5 CRC64;
                                SEQUENCE FROM N.A.
STRAIN=OT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Dna2-nam7 helicase family protein.
MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=PF0572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8U398;
                                                                                                                                                  NCBI_TaxID=53953;
                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Thermococci;
                                                                                                                                                                                                                                                                        Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2261;
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8; Conserv
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80.0%;
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Pred. No. 6.5;
0; Mismatches
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Pred. No.
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6.5;
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A. Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A. Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A. Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A. Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
A. Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A. Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A. Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A. Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A. Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A. Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A. Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A. Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A. Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A. Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A. Wincker P., Souciet J.L.,
                       Query Match
Best Local
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Matches
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Q6FKP9;
Q5-UUL-2004 (TrEMBLrel. 27, Created)
Q5-UUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|P34243 Saccharomyces cerevisiae YKL017c DIP1.
ORFYNames=CAGL0109735g;
ORFYNames=CAGL0109735g;
ORFYNames=CAGL0109735g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 5:55-0012003.1; -.
EMBL; AP000004; BAA30003.1; -.
PIR; E71080; E71080.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003577; F:DNA binding; IEA.
InterPro; IPR004483; put DNA helic.
TIGRFAMB; TIGR00376; put DNA helic; 1.
Complete proteome; DNA-binding; Hypothetical protein.
Complete proteome; DNA-binding; Hypothetical protein.
                                                                                                                                                                                                                                                                                                          "Genome evolution in yeasts.";
Nature 430:35-44(2004).
EMBL; CR380958; CAG62165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=CBS138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masuchi Y. Shizuya H., Kikuchi H.; "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76(1998)
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Sakai M., Ogura K., Otsuka R.,
Funahashi T., Tanaka T., Kudoh
Aoki K.-I., Yoshizawa T., Kutaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                       GO; GO:0005524; F:ATP binding; GO; GO:0003677; F:DNA binding;
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                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                         InterPro; IPR011545; DEAD/DEAH
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                                                                                                           SM00487; DEXDC; 1. -
Ms; TIGR00376; put_DNA_helic; 1.
CE 695 AA; 78391 MW; DC4995FE4CD0B420 CRC64;
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Similarity 7; Conserv
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                                                                                                                                            IPRO04483; put DNA_helic.
00487; DEXDc; 1.
TIGR00376.
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  .Conservative
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                       86.4%;
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Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
nuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Nakamura Y., Robb F.T., Horikoshi K.,
Score 38; DB
Pred. No. 6.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
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Pred. No.
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6.5;
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6.9;
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horikoshii OT3.";
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QPEQNE QPEQNE AC QPEQNE QP
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Q9EQN5;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                              Q60560;
01-NOV-1997
                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 45, Last sanutation update)
05-JUL-2004 (Rel. 48, Last annotation update)
DNA-binding protein SMUBP-2 (Immunoglobulin MU binding protein 2)
(SMUBP-2) (Insulin II gene enhancer-binding protein) (RIPE3B-binding complex 3B2 Pl10 subunit) (RIP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miao M., Chan S.L., Fletcher G.L., Hew C.L.;
"The rat ortholog of the presumptive flounder antifreeze enhancer-
binding protein is a helicase domain-containing protein.";
Bur. J. Biochem. 267:7237-7246 (2000).
BURL; AF19911; AG28561.1; -
                                                                                                                                                          Name-IGHMBP2; Synonyms-RIP1, SMUBP2;
Mesocricetus auratus (Golden hamster).
Bukaryota, Metazoa; Chordata, Craniata; Verrebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000058; Znf_AN1.
Pfam; Pro1424; R3H; 1.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
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STRAIN-Sprague-Dawley;
MEDLINE-20558263; PubMed-11106437;
Miso M., Chan S.L., Fletcher G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMB2 MESAU
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                        SEQUENCE FROM N.A. TISSUE-Insulinoma;
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SMART; SM00154; ZnP_AN1; 1.
TIGRPAMB; TIGR00376; put_DNA_helic; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence)
01-MAR-2004 (TrEMBLrel. 26, Last annotat.)
Antifreeze-enhancer binding protein AEP.
  MEDLINE=95394901; PubMed=7665561; DOI=10.1074/jbc.270.37.21503;
                                                                                                   NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000357; F:DNA binding; IEA.
GO; GO:0000166; F:nucleotide binding;
InterPro; IPR003593; AAA ATPase.
InterPro; IPR011545; DEAD/DEAH N.
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PIR; T48845; T48845.
HSSP; P38935; 1MSZ.
InterPro; IPR004483; put DN
InterPro; IPR001374; R3H.
Pfam; PF01424; R3H; 1.
                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=93352537; PubMed=8349627;
MEDLINE=93352537; PubMed=8349627;
Pukita Y., Mizuta T.-R., Shirozu M., Ozawa K., Shimizu A.,
Pukita Y., Mizuta T.-R., Shirozu M., Ozawa K., Shimizu A.,
"The human S mu bp-2, a DNA-binding protein specific to the
"The human S mu bp-2, a Guence related to the immunoglobul"
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DOMAIN
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Mammalia; Butheria;
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                                   SEQUENCE FROM N.A.
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MEDLINE=99160766; PubMed=10049831; DOI=10.1006/viro.1998.9588;
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Activator; ATP-binding; DNA-binding;
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-I- FUNCTION: Binds to the insulin II gene RIPE3B enhancer region.
-I- SUBUNIT: Composed of at least three polypeptides: p58, p62, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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SUBCELLULAR LOCATION: Nuclear (Potential)
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Primates;
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Poly-Val.
SS DNA-binding (By & Gln/Pro-rich.
Poly-Ly8.
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Pred. No. 10;
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; 9489671B46DAD04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (Potential).
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o the single-
bulin mu chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology
[3]
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"Smubp-2 i
                                                             TURN
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TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Ľ14754; AAA53082.1; -.
EMBL; Ľ24544; AAA70430.1; -.
EMBL; M64979; AAA58611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                SEQUENCE
                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                   TIGRFAMs; TIGR00376; put_DNA helic; 1.
3D-structure; Activator; ATP-binding; DNA-binding; Helicase;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01424; R3H; 1.
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004483; put_DNA_helic.
InterPro; IPR001374; R3H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1MSZ; NMR; A=709-794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A47500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A recombinant cDNA derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91340730;
            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 266:15876-15881(1991).
                                                                                                                                                                                                                                                                                                                                                                                               GO:0006281; P:DNA repair; TAS.
GO:0006260; P:DNA replication; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: In all tissues examined. SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurotropic virus JCV.
SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: In all tissues examine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0003697; F:single-stranded DNA bin GO:0006310; P:DNA recombination; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0003678; F:DNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DNA-binding protein specific to 5'-phosphorylated single-stranded guanine-rich sequence related to the immunoglobulin mu chain switch region. Preferentially binds to motif (5'-GGGCT-3'). Stimulates the transcription of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:5542; IGHMBP2.
Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Wang Y.C., Montalvo E.A.;
represses the Epstein-Barr virus lytic switch promoter.";
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                                                 AΑ;
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                                                                                                                                                                                                                                                                                                                         protein;
           86.4%;
                                                 109095 MW; A5895892534D8841 CRC64;
Score 38; DB
Pred. No. 10;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   activity; TAS.
led DNA binding;
                                                                                                                                                              ㅂㅈ
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(in Ref. 2)
(in Ref. 2)
(in Ref. 2)
> GGRV (in Ref. 2)
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                         Length 993;
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RESULT 14
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P40694;
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DOMAIN
                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as lor modified and this statement is not removentities requires a license agreement (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/c; TISSUE-Spleen;
MEDLINE-93261806; PubMed-8493094;
Mizuta T.-R., Fukita Y., Miyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinforthe European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                            motif (5'-GGGCT-3').
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: In all tissues examined.
-!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Ighmbp2; Synonyms=Smbp-2, Smbp2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
01-FEB-1995
                                                                                          SEQUENCE
                                                                                                                                                                                  LIUKFAMB; TIGRO0376; put DNA helic; 1.
Activator; ATP-binding; DNA-binding; Helicase; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                                                          Pfam; PF01424; R3H; 1
                                                                                                                                                                                                                                    MGD; MGI:99954; Ighmbp2.
InterPro; IPR004483; put
InterPro; IPR001374; R3H
                                                                                                                                                                                                                                                                                              EMBL; L10075; AAA40143.1;
                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                      ISSP; P38935; 1MSZ
                                                                                                                                                                                                                                                                                   PIR; S35633; S35633.
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                                                        Similarity
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                       ILAGDXXQLP 12
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104 (Rel. 44, Last amnotation update)
105 protein SMUBP-2 (Immunoglobulin MU binding
106 (Cardiac transcription factor 1) (CATF1).
 ILAGDHRQLP
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SS DNA-binding (By simils Gln/Pro-rich.
Poly-Lys.
Poly-Lys.
The localization si
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                                             0;
                                             Score 38; DB Pred. No. 10; 0; Mismatches
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(See http://www.isb-sib.ch/announce/
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RP SEQUENCE FROM N.A.

RR Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Galagan J.E., Calvo S.E., Smirnov S., Purcell S., Rehman B.,

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

RA Cui D., Ianaklev P., Pedersen D., Nelson M., Washburne M.,

RA Qui D., Ianaklev P., Pedersen D., Nelson M., Washburne M.,

RA Cothe G.O., Jedd G., Meweś W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Meweś W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Meweś W., Staben C., Marcotte E., Greenberg D.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R.C., Rudd S., Frishman D.,

RA Kamal M., Kamyysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Soliter S., Dunlap J., Radford A., Aramayo R.,

RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

RI Nature O.O-0(2003).

C. EmBL/Genisank/DDBJ whole genome shotgun (WGS) entry which is

CC EmBL; AABX01000237, EAA32579.1; -.
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7S8B9 PRELIMINARY; PRT; 1190 AA.
Q7S8B9;
Q1-MAR-2004 (TrEMBLrel. 26, Created)
O1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 1190 AA; 132937 MW; E3C5DF5A853E20A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. Name=NCU06627.1;
                                                                                                    818 ILAGDVKÓLP 827
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                                                                                                                                   ILAGDXXQLP 12
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                          86.4%;
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                                                                                                                                                                                                                          Score 38; DB 2; Length 1190; Pred. No. 12;
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AAY77813
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79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	Ņ	82.4
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Aar66935	Abu20507	Aag17781	Adp44131	Abw01205	Aay77814	Aag17782	Ads15016	Abu38555	Aau36323	Abm67220	Abu40377	Abo68442	Abu39332	Aar66937	Aam83885	Adf05324	Aae38309	Aaw03665	Aay21377
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ALIGNMENTS

AAY77813 standard; peptide;

Yeast Mttl protein fragment.

AAY77813; 31-MAY-2000

(first entry)

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KW Helicase B; HCSB; MTT1; modulator of translation termination; eRF1;
KW eukaryotic release factor; peptidyl transferase; beta-thalassemia;
KW beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
KW helicase.
XX
Q3-FBB-2000.
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22-JUL-1999; 99WO-US016802.
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22-JUL-1999; 98US-00120435.
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22-JUL-1998; 98US-00120435.
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21-JUL-1998; 98US-00120435.
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WPI; 2000-171458/15.

PT New multiprotein complex which can modulate peptidyl transferase activity of during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.

XX Example 1; Fig 1; 89pp; English.

XX Example 2; Fig 1; Fig 1;

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cc involving a defect in the complex, by transfecting cells with encoding cnucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved in cell transfers experience activity during translation, inhibiting the competidyl transferse activity during translation, inhibiting the contermination. Vectors comprising polynucleotides encoding translation cells to termination. Vectors comprising polynucleotides encoding the complex (or continued with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant conditions and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferse activity during translation translation of cells. They care also useful to modulate the efficiency of translation translation of cells. They care also useful to modulate the efficiency of translation of aberrant compositions modulating binding to MTTI, useful to identify genes.

CC Sequences AAY7813-817 represent protein fragments from yeast superfamily
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Best Local
                                                                                                                                                                                    Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mttl.
                 The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6630294-B1
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antiviral therapy
                                                                                                                                                Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9908-00359268
and for suppression
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77.8%;
                                                                                                                                            Opp; English.
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Pred. No. 1.3e+02;
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  of pathological nonsense mutations
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                   The invention relates to a method of identifying a test composition that CC modulates the efficiency of translation termination comprising contacting Ct the RNA helicase MTT1 with a composition or agent under conditions CC permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1. The CC composition and methods are useful for modulating the fidelity of CC translation termination or for identifying agents that: affect the CC translation termination event, promote degradation of aberrant C transcripts, and provide modulators (inhibitors/stimulators) of peptidyl C transferase activity during initiation, elongation, termination amany activity during initiation, elongation, termination and mRNA degradation of translation. The agents, which may be antagonists or agonists, are useful in screening, diagnostic and therapeutic purposes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a test composition or agent that modulates the efficiency translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PELT/)
(CZAP/)
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22-JUL-1999;
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7; Conserva
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CZAPLINSKI K.
DINMAN J D.
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99US-00359268
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Pred. No. 1.3e+02;
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Matches 7
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                                                       The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide
                                                                                                                                                                                                                                                                                                                                           Identifying an agent that increases nonsense suppression, fo therapy, by contacting modulator of translation termination Saccharomyces cerevisiae with a test agent, and detecting sp binding to Mttl.
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                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (-SNAS)
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of translation termination; MTT1; helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Czaplinski K,
                                                                                                                                                                                                                                                                                   Col 43;
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Pred. No. 1.3e
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Best Local
                                                                        The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting the RNA helicase MTI1 with a composition or agent under conditions permitting binding between the MTI1 and the composition, detecting specific binding of the test composition or agent to the MTI1, and determining if the test composition or agent inhibits the MTI1. The composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, permit monitoring of a termination event, promote degradation of aberrant transcripts, and provide modulators (inhibitors/stimulators) of peptidyl reansforms activity divide modulators (inhibitors/stimulators) of peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a test composition or agent that translation termination comprises contacting composition or agent, and determining if the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia, beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschaprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2004
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                           transferase activity during initiation, elongation, degradation of translation. The agents, which may be
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 37; SEQ ID NO 5; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-449400/42
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22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibits
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(CZAP/) CZAPL:
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CZAPLINSKI
DINMAN J D.
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99US-00359268.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  test composition or agent
      may be antagonis and therapeutic
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            n, termination and mRNA be antagonists or theraponist
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                                                    The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                           New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicase B; HCSB; MTT1; modulator of translation termination; eRF1 eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.
   transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions
                                                                                                                                                                                                                                         Claim 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200005586-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LXXSLFERV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motif V.
                                                                                                                                                                                                                                                                                                                                                                                                                          VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LXXSLFERV 9
                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                    Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        NEW JERSEY
                                                                                                                                                                                                                                       79; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00120435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US016802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "reisdues indicated Xaa
                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                        Dinman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Le
1.8e+06;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eRF1; eRF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABW01186 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                Identifying an agent that increases nonsense suppression, fo
therapy, by contacting modulator of translation termination
Saccharomyces cerevisiae with a test agent, and detecting sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABW01186
                                                                                                                                                                    Peltz S,
                                                                                                                                                                                                                          22-JUL-1998;
                                                                                                                                                                                                                                                     22-JUL-1999;
                                                                                                                                                                                                                                                                                                            US6630294-B1
                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulator of translation termination; MTT1; helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             involving a defect in the complex, by transfecting cells with encoding
                                                                                                                                         WPI; 2003-810549/76
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                                                                     to Mttl
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                                                                                                                                                                    Czaplinski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerevisiae consensus motif peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      nonsense
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                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     /label= Unknown
/note= "Xaa may
                                                                                                                                                                                                 JERSEY
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                                                                                                                                                                                                MEDICINE & DENTISTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation; yeast.
                                                                                                                                                                      Dinman
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                        amino
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5.7;
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                                                                                                               for
                                                                                   specific
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                                                                                                               antiviral
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The invention relates

to a method of identifying by contacting modulator of

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; beta-globin; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae consensus motif peptide.
The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting the RNA halicase MTT1 with a composition or agent under conditions permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1, and determining if the test composition or agent inhibits the MTT1. The composition and methods are useful for modulating the fidelity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                    Identifying a test composition or agent that
translation termination comprises contacting
composition or agent, and determining if the
inhibits the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast translation
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                                                                                                                                                                                                                                         Disclosure; SBQ ID NO 10; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-449400/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DINM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PELT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELTZ S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DINMAN J D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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99US-00359268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dinman JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulation protein related
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5.7;
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                                                                                                                                                                                                                                                                                                                              modulates the efficiency of
the MTT1 with the test
test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   functional activity of mRNAs by altering frameshift frequency, permit cc monitoring of a termination event, promote degradation of aberrant cc transcripts, and provide modulators (inhibitors/stimulators) of peptidyl ctransferase activity during initiation, elongation, termination and mRNA cc degradation of translation. The agents, which may be antagonists or cagonists, are useful in screening, diagnostic and therapeutic purposes, cc for diseases or conditions resulting from or cause premature translation, cc such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular controlled to the major of the minor controlled to the controlled squence of a yeast translation termination modulation controlled to reference is made to it in the main body of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                      Identifying an agent that increases nonsense suppression, for therapy, by contacting modulator of translation termination saccharomyces cerevisiae with a test agent, and detecting spaceharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABW01195 standard;
                                                                                                   Disclosure;
                                                                                                                                                                                                                  Peltz S,
                                                                                                                                                                                                                                                                    22-JUL-1998;
                                                                                                                                                                                                                                                                                                                       07-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                 therapy; HCSB;
                                                                                                                                                                                                                                                                                                                                                                                                               Modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABW01195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, per
                                                                                                                          binding to Mttl.
                                                                                                                                                                                                                                                                                              22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                              VIND
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                                                                                                                                                                                                                Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                  Col 47; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
                                                                                                                                                                                                                                              MEM
                                                                                                                                                                                                                                                                                                                                                                                                               translation termination; MTT1; helicase B; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae consensus peptide
                                                                                                                                                                                                                                                                                                                                                                         cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                   nonsense mutation;
                                                                                                                                                                                                                                                                      98US-0093685P
                                                                                                                                                                                                                                                                                              99US-00359268
                                                                                                                                                                                                                                              JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%;
                                                                                                                                                                                                                                            MEDICINE & DENTISTRY
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Pred. No. 5
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The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae consensus peptide

និងនិង្គិនិងនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង្គិនិង

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Best Local S
Matches 6
                                                         the RNA helicase MTT1 with a composition or agent under conditions permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1 and detecrmining if the test composition or agent inhibits the MTT1. The composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, permit monitoring of a termination event, promote degradation of aberrant transcripts, and provide modulators (inhibitors/stimulators) of peptidyl transferase activity during initiation, elongation, termination and mRNA degradation of translation. The agents, which may be antagonists or agonists, are useful in screening, diagnostic and therapeutic purposes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent inhibits the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis;
Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa;
Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-fihalassaemia; beta-globin; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-2004
                                   agonists, are useful in screening, for diseases or conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 19; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-449400/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CZAPLINSKI K.
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99US-00359268.
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100.0%; Pr
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   resulting from or cause premature translation, beta-globin, Duchenne/Becker Muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
Pred. No.
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                   The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe tha hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome derived single exon protein #4394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression analysis, for a splicing events, for assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2002; 2002US-00029386
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HANZEL D K.
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alteration.
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ORF-encoded

peptide

comprising

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RESULT 12
ABO78875
ID 78875
AC ABO78
XX ABO78
XX Pseud
PF 18-FE
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PF 18-FE
PR 27-JI
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Best Local
  The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosts and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
                                                                                                                                        Disclosure;
                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                          Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial infection; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa polypeptide #11050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB078875;
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6; Conserv
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                                                                                                                                        SEQ
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98US-0094190P.
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                                                                                                                                     27621; 455pp; English
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Pred.
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826

aeruginosa polypeptides

of the

Note: The

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

WPI; 2003-615309/58.

Rubenfield MJ,

Nolling J,

Deloughery

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Bueh

(GENO-) GENOME

THERAPEUTICS CORP 98US-0074788P. 98US-0094190P.

N-PSDB;

ABD14181.

18-FEB-1998; 27-JUL-1998;

Disclosure; SEQ ID NO 29356; 455pp; English

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at secretars are represented.
                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa polypeptide #12785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2004 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB080610;
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                       99US-00252991
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Pred. No. 3.46
1; Mismatches
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RESULT 14
ABO63671
ID ABO63671
XX ABO63
AC ABO63
XX AC ABO63
XX AC ABO63
XX Recom
KW Recom
KW
RESULT 15
ABU52076
ID ABU52
XX
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid permally linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                              ABU52076 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 298
                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                               LXXSLFER 8
                                                                                                                                                              LSASLFER 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10188; 932pp; English.
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                     AA;
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75.0%;
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Pred. No.
                                                                                                                                                                                                                                                                Score 28; DB 7; Le
Pred. No. 4.3e+02;
0; Mismatches 2;
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3.8e+02;
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                                                                                                                      The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to represent an illegible residue
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밁 á RESULT 2 US-09-248-796A-19347 US-09-359-268A-25 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-07 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2. SEQ ID NO 25 RESULT 1 US-09-359-268A-25 GENERAL INFORMATION: APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS TILE REFERENCE: 107196.132 CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR APPLICATION NUMBER: US 60/076,409 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 19347 Sequence 19347, Application US/09248796A Patent No. 6747137 Matches GENERAL INFORMATION: Sequence 25, Application Patent No. 6630294 Best Local Query Match APPLICANT: I APPLICANT: I FILE REFERENCE: 601-1-85N CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22 APPLICANT: Czaplinski, Kevin APPLICANT: Dinman, Jonathan; TITLE OF INVENTION: A SUBPAM, TITLE OF INVENTION: THE FIDE TITLE OF INVENTION: THEREOF LENGTH: 415 TYPB: PRT ORGANISM: Baccharomyces cerevisiae 193 1 LXXSLFERV 9 7; Conservative Similarity LETSLFERV 201 PatentIn Ver. 2.0 Stuart 1998-07-22)S: 32 91.2%; A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES US/09359268A 60/093,685 Score 31; Pred. No. Mismatches DB 23; 4 Length 415; Indels 0 Gaps TO CANDIDA ALBICAN 0

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LENGTH: 10
TYPE: PRT
ORGANISM: saccharomyces cerevisiae
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LENGTH: 9
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
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                                                                                                              CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22 PRIOR APPLICATION NUMBER: 60/093,685 PRIOR FILING DATE: 1998-07-22 NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                    APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
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TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                          FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
OTHER INFORMATION: Xaa = any amino acid
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9; Conserv
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                                                                                                     PatentIn Ver. 2.0
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100.0%;
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k; Pred. No. 4.1
0; Mismatches
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hes 0;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wegand, Roger C.
FITTE OF INVENTION: Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION UMMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
FRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11930
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US-09-359-268A-19
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US-09-902-540-11930
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Best Local S
Matches 8
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CURRENT FILING DATE: 1999-07-22.
PRIOR APPLICATION NUMBER: 60/93,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                    Matches
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                                                Best Local Similarity
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Best Local Similarity
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APPLICANT: Hinkle, Gregory
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                                                                                                                TYPE: PRT ORGANISM: Myxococcus xanthus
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                                                                                                                                                LENGTH: 195
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     1 LXXSLFERV 9
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                                                  82.4%;
66.7%;
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100.0%; Pred. No. 4.1e+05;
... Mismatches 0;
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                                    1; Mismatches
                                                   Score 28;
Pred. No.
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Pred. No. 0.8;
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US-09-489-039A-10188
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US-09-252-991A-27621
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GENERAL INFORMATION:
APPLICANT: Marc J. F
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SEQ ID NO 27621
LENGTH: 230
                                                         Sequence 10188, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
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LENGTH: 260
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APPLICANT: Marc J.
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Patent No. 6551795
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CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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66.7%;
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Pred. No.
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US-08-724-354D-4
                                                                                                                                    US-08-724-354D-4
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SEQ ID NO 10188
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Matches 6; Conserve
                                                                 Matches
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASHSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
FILING DATE: 29-APR-1996
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PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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TYPE: PRT
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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STREET: 42...
CITY: La Jolla
CTATE: CA
TICA
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                      B2.4%; Focal Similarity 66.7%; Local Similarity 66.7%; hes 6; Conservative
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037
                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
603 LSQSLFERL 611
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                               LXXSLFERV 9
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                                                                                                                                                                                                   1043 amino acids
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75.0%;
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Pred. No. 81;
                                                                                  Score 28; DB 2;
Pred. No. 3e+02;
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                                                                                                 DB 2;
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RESULT 11 US-09-270-984A-4

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                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08724354D Patent No. 5994119
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APPLICANT: Dietz, Harry C.
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             Cli.
STATE:
COUNTRY: USA
COUNTRY: USA
70, 92037
           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/724,354D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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APPLICATION NUMBER:
FILING DATE:
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 4225 Excutive Square,
                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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APPLICATION NUMBER: US/09/270,984A
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CORRESPONDENCE ADDRESS:
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STREET:
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nes 6; Conserv
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FILING DATE: 01-OCT-1996
                                                           OPERATING SYSTEM:
                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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4225 Excutive Square, Suite 1400
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                                                         IBM Compatible
SYSTEM: Windows95
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66.7%;
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                                                                                                                                                                                       P.C.
Suite 1400
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Query Match
Best Local Similarity
6; Conserve
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US-09-270-984A-2
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                                                                            US-09-270-984A-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                   NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
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LENGTH: 1118 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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STATE: CA
COUNTRY: USA
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Local Similarity 66.7%;
tes 6; Conservative
                                                                                                                       TYPE: amino acid
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                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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REGISTRATION NUMBER:
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                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
SYSTEM: Windows95
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                           82.4%;
66.7%;
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                           Pred.
                             Score 28; DB 3;
Pred. No. 3.2e+02;
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Pred. No. 3.2e+02;
                 Mismatches
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                                           Length 1118;
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              Gaps
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-10116
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SEQ ID NO 10116
LENGTH: 1140
TYPE: PRT
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Matches 6; Conserv
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Patent No. 681233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLUHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 20701
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
PILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                          STREET: 415
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, DANIE!
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                               COUNTRY: U
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Pred. No. 3.3e+02;
1; Mismatches 2; Indels
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Query Match
Best Local Similarity
""" hes 6; Conserve
Search completed: April 18, 2005, 08:18:34 Job time : 11.2336 secs
                                                        문
                                                                                 ફ
                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-930-996A-4
                                                                                                                                                                                                                                                   FILING DATE: 13-APR-1
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                         LENGTH:
                                                        472 SLFERV 477
                                                                            4 SLFERV 9
                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                           1240 amino acids
                                                                                                            Conservative
                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                  13-APR-1995
                                                                                                                           82.4%; Score 28; DB 3; L
100.0%; Pred. No. 3.6e+02;
                                                                                                              <u>.</u>
                                                                                                               Mismatches
                                                                                                               0; Indels
                                                                                                                                        Length 1240;
                                                                                                              0,
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
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34
1 LXXSLFERV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   April 18, 2005, 08:06:16; Search time 31.927 Seconds (without alignments) 93.693 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa
2: /cgn2_6/ptodata/1/pubpaa
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/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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2 6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*
2 6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
2 6/ptcdata/1/pubpaa/USO6_PUBCOMB.pep:*
2 6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                          6/prodata/1/pubpaa/PCTUS PUBCOMB.pep:*
6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21 55 66 76 11 11 11 11 11	Regult No.
31 30 30 30 30 30 30 30 30 30 30 30 30 30	Score
78888888888	Query
415 415 10 10 7 71 199 638 831 935 935 935 1118	Query Match Length DB
166111611161116111611116111111111111111	BB .
US-10-652-334-5 US-10-652-334-10 US-10-652-334-10 US-10-652-334-19 US-10-652-334-19 US-10-652-334-19 US-10-629-386-31794 US-10-629-386-318690 US-10-424-599-205643 US-10-369-493-18631 US-10-369-493-2087 US-10-409-765A-1706 US-10-409-765A-1706 US-10-409-765A-1706 US-10-409-765A-1706	ID
Sequence 25, Appli Sequence 5, Appli Sequence 10, Appli Sequence 19, Appli Sequence 31794, A Sequence 38822, A Sequence 181690, Sequence 208643, Sequence 2087, Ap Sequence 2087, Ap Sequence 1706, Ap Sequence 1706, Ap Sequence 6, Appli Sequence 67256, A	Description

RESULT 2

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
26	26	26	26	26	26	26	26	26	26	26	26	26	26	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
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348	324	323	314	312	308	296	281	273	269	175	158	124	77	2593	2462	992	971	971	890	839	651	644	604	413	380	333	333	333	304	298	286
16	10	14	16	16	15	16	16	16	16	16	15	15	15	16	16	15	16	15	16	14	15	5	15	15	16	15	15	φ	16	15	16
-10	US-09-905-290A-4	US-10-304-928-8	US-10-437-963-162020	US-10-767-701-46662	-10-282-122A	US-10-437-963-153126	US-10-437-963-141996	US-10-767-701-44666	-10-767-701-	US-10-767-701-46637	US-10-369-493-9883	US-10-282-122A-61519	US-10-424-599-180332	US-10-437-963-114115	US-10-437-963-114113	US-10-369-493-12790	US-10-451-467A-698	US-10-369-493-1715	-10-437-963-	-10-032	US-10-335-977-8440	US-10-335-977-8439	-10-282	US-10-282-122A-48431	US-10-652-334-29		US-10-282-122A-66479	0	US-10-437-963-173847		US-10-437-963-142655
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132857,	4, Appli	8, Appli	162020,	46662, A	49263, A	153126,		0	,0	46637, A	•	61519, A	180332,	114115,	114113,	12790, A	•	1715, Ap	118530,	7124, Ap		8439, Ap	58045, A	48431, A	29, Appl	571, App	56479, A	11916, A	173847,	68301, A	5

ALIGNMENTS

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Baccharomyces cerevisiae
US-10-652-334-25
밁
           გ
                           Matches
                                 Query Match
Best Local
193 LETSLFERV 201
            1 LXXSLFERV 9
                          Similarity 7; Conserv
                           Conservative
                                 91.2%;
77.8%;
                           0,
                           Score 31; DB 16; Length 415; Pred. No. 1.1e+02; O; Mismatches 2; Indels
                           0,
                            Gaps
                            0
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PILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR APPLICATION NUMBER: 05/09/359,268A
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
PRIOR PILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTING DATE: 2.0
SEQ ID NO 10
LENGTH: 10
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                                    S
                                                                                                                                                                             ; OTHER INFORMATION: Xaa = any amino acid
US-10-652-334-10
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                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JENERAL INFORMATION:
APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/359,268A PRIOR FILING DATE: 1999-07-22
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CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
                                                                                                                                                                                                                      ORGANISM: saccharomyces cerevisiae FEATURE:
                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
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                                           LXXSLFERV 9
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No. US20040115787A1
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                                                                                       Conservative
                                                                                                          88.2%;
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100.0%; Pred. No.
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                                                                                     0; Mismatches
                                                                                                          Score 30; DB 16;
Pred. No. 4.8;
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                                                                                                                              Length 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-652-334-19
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL DAVID K.
APPLICANT: HANZEL DAVID K.
APPLICANT: HANZEL DAVID K.
APPLICANTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 7
                                                                                                Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31794, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                               Matches
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Best Local
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CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPAMILY OF RNA HELICASES
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                            OTHER INFORMATION: MAP TO AC003972.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
OTHER INFORMATION: SWISSPROT HIT: Q09820, EVALUE 2.00e-24
                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100.0%; 6; Conservative
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                                       LXXSLFERV 9
  LSQSLFERL 32
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                                                                               Conservative
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                                                                                                82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%;
                                                                             Score 28; DB Pred. No. 91; 1; Mismatches
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Pred. No.
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                                                                                                                       14;
                                                                               2
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                                                                                                                   Length 71;
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RESULT 8
US-10-424-599-205643
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181690
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 181690, Application US/10437963 Publication No. US20040123343A1
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SEQ ID NO 38822
LENGTH: 199
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                                                                                                                                                                                             Query Match
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILLING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(638)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7426_1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT4530_7893C.1.pep
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                           Watch 82.4%;
Local Similarity 66.7%;
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                                                                              LAOSLPERL 84
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Barbazuk, Brad
                                                                                                                                                              Conservative
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66.7%;
                                                                                                                                                                               Score 28; DB 16; Length 638; Pred. No. 8e+02;
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Pred. No. 2.5e+02
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RESULT 10
US-10-369-493-2087
; Sequence 2087, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 205643

LENGTH: 774
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18631
LENGTH: 821
TYPE: PRT
ORGANISM: Halobacterium sp. NRC-1
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                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Green, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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APPLICANT: Hink
APPLICANT: Slat
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LOCATION: (1)..(734)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
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Local Similarity 66.7%;
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66.7%;
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Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                   Length 821;
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RESULT 12
US-10-474-553-6
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US-10-408-765A-1706
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US-10-408-765A-1706
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              Sequence 6, Application US/10474553

Publication No. US20040161765A1

GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING DISEASE
TITLE OF INVENTION: GENES USING NONSENSE-MEDIATED DECAY INHIBITION
FILE REFERENCE: JHV-020.25
CURRENT APPLICATION NUMBER: US/10/474,553
CURRENT FILING DATE: 2003-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1766
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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FULE REFERENCE: 38-10(52052)B
CURRENT FLING DATE: 2003-02-28
PRIOR APPLICATION: 2003-02-28
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PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2087
LENGTH: 925
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WAITHOCK, DAILE B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
PRIOR APPLICATION NUMBER: 60/283,920
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Local Similarity 66.7%;
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Gibson, Bradford W.
Taylor, Steven W.
Glenn, Gary M.
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Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
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Query Match Best Local

Local Similarity

79.4**%**; 75.0**%**;

Length 210;

Indels

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Gaps

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Score 27; DB 15; Pred. No. 4.4e+02; 0; Mismatches 2.

6,

Matches

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RESULT 13
US-10-282-122A-67256
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-553-6
US-10-282-122A-67256
                                                                         SEQ ID NO 67256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
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Publication No. US20040029129A1
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                                                                                         Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Chery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/242,578
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                ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                      LENGTH:
                                                                                                                                                                                                          APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                FILING DATE:
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FILING DATE: 2000-0
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Zyskind, Judith
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Yamamoto, Robert
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,337

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347
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US-10-282-122A-68301
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SEQ ID NO 142655
LENGTH: 286
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_43640C.1.pep
US-10-437-963-142655
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US-10-437-963-142655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.4%;
Best Local Similarity 55.6%;
Matches 5; Conservative
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT:
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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Barbazuk, Brad
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Pred. No. 6e+02;
2; Mismatches
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LENGTH: 298
                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Pseudomonas putida
                                                                                                                                                        TOCAL Similarity 55.6%; Local Similarity 55.6%; es 5; Conservative
                                                                                   49 LSHSLFQRI 57
                                                                                                                               1 LXXSLFERV 9
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Pred. No. 6.3e+02;
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34
1 LXXSLFERV 9
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		replication licens	hypothetical prote	ribonuclease II fa	pro		Kina	hypothetical prote	conserved hypothet	hypothetical prote	protein B0361.7 (i	probable alcohol [histidinol-phospha	probable pyruvate	protein T07E3.3 [i	OAC2 protein - Azo	hypothetical prote	hypothetical prote	resistance complex		hypothetical prote	DNA helicase [impo	virulence associat	DNA-damage-inducib	cyclopropane fatty	pane-	probable permease	DNA dependent ATPa	Description

RESULT 2 H83606

probable permease of ABC transporter PA0313 [imported] - Pseudomonas aeruginosa (strain

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metabolite transpo T1N6.17 protein - hypothetical prote	probable Arac-type probable na+/h+ an probable ATPase mr hypothetical prote	chitinase (EC 3.2. hypothetical prote transcription regu cysteine synthase	hypothetical prote probable lipoate p conserved hypothet hypothetical prote probable transcrip

ALIGNMENTS

DNA dependent ATPase/DNA helicase B - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YER176w C;Species: Saccharomyces cerevisiae C;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 09-Jul-2004 C;Accession: S30862; S50679; JC2490; PC2368 R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993 밁 ঠ submitted to the EMBL Data Library, December 1994 A;Description: The sequence of S. cerevisiae cosmids 9163 and 9132. A;Reference number: S50679 A;Accession: S50679 A;Map position: 5R C;Keywords: nucleotide binding; P-loop F;670-677/Region: nucleotide-binding motif A (P-loop) A;Cross-references: SGD:S0000978; MIPS:YER176w A; Gene: SGD: ECM32 C;Genetics A;Molecule type: protein A;Residues: 277-283;623-633,'X',635-643 <BI2> C;Comment: This enzyme plays pivotal roles in R;Biswas, B.B.; Chen, P.H.; Leszyk, J.; Biswas, S.B. Biochem. Biophys. Res. Commun. 206, 850-856, 1995 A;Title: Biochemical and genetic characterization of a replication protein A dependent A;Reference number: JC2490; MUID:95134267; PMID:7832796 A;Molecule type: DNA A;Residues: 1-1121 <DIE> A;Cross-references: EMBL.U18922; NID:g603405; PIDN:AAB64703.1; PID:g603417; MIPS:YER176w A;Molecule type: DNA A;Residues: 1-1121 <MUL> A; Reference number: S30812 A; Accession: S30862 A; Accession: PC2368 A;Cross-references: UNIPROT: P32644; GB: U18922; EMBL: L11229; NID: g603405; PIDN: AAB64703.1 A; Molecule type: DNA \;Residues: 1-1121 <BIS> Matches Query Match Accession: JC2490 Local 960 1 LXXSLFERV 9 Similarity 77. LETSLPERV 868 91.2**%**; Score 31; DB Pred. No. 50; 0; Mismatches DB 2; Length 1121; the unwinding of the DNA double helix duri 2; Indels 0 Gaps 0

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C;Accession: AC2819
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: H83606
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                      RESULT 4
D97597
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C;Date: 15-Sep-2000 #sequence_rev
C;Accession: H83606
                                            R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                              cyclopropane fatty acyl phospholipid synthase (AE005389) [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: D97597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AC2819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyclopropane-fatty-acyl-phospholipid synthase [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A;Reference number:
A;Accession: D97597
              A; Title: Genome Sequence of A; Reference number: A97359;
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A;Accession: H83606
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                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues: 1-341 <KUR>
;Residues: 1-341 <KUR>
;Residues: Dipror:Q8UDZ2; GB:AE008688; PIDN:AAL42969.1;
;Cross-references: UNIPROT:Q8UDZ2; GB:AE008688; PIDN:AAL42969.1;
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Best Local
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100.0%;
              the Plant Pathogen and Biotechnology Agent Agrobacterium tum MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                                                              Mismatches
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                                                              Miller, N.; Blanchard, N
Doughty, D.; Scott, C.;
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                                                              M.; Qurollo, ; Lappas, C.;
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K.; Lim,
                                                                                  Goldman
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C;Genetics:
A;Gene: BH1150
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A; Residues: 1-451 <STO>
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKelson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Bodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64675
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A;Residues: 1-341 <KUR>
A;Cross-references: UNIPROT:Q8UDZ2; GB:AE007869; PIDN:AAK87733.1; PID:g15157098; GSPDB:GN
C;Genetics:
A;Gene: AGR_C_3595
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                 virulence associated protein homolog - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Nug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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A;Experimental source: strain C-125
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Nucleic Acids Res. 28, 4317-4331, 200
A;Title: Complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-damage-inducible protein BH1150 [imported] - Bacillus halodurans (strain C_1Species: Bacillus halodurans
                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83793
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                                                                                                                     ;Cross-references: UNIPROT:P56123;
;Superfamily: virulence-associated
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LXXSLFERV 9
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28, 4317-4331, 2000
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Pred. No.
                                                             Score 28; DB 2;
Pred. No. 1.4e+02;
                                                                                                                        GB:AE000630;
protein vacB
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A;Cross-references: UNIPROT:Q09820; EMBL:Z54366; NID:g1019812; PIDN:CAA91194.1; PID:g132 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995 A;Reference number: Z21745 A;Reference number: Z21745 A;Recession: T37779
nonsense-mediated mRNA decay trans-acting factor - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T43280
                                                                                       RESULT
T43280
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A;Molecule type: DNA
A;Residues: 11-935 <BA2>
A;Cross-references: EMBL:Z54366; PIDN:CAA91194.2; GSPDB:GN00066; SPDB:SPAC16C9.06c
A;Cross-references: strain 972h-; cosmid c16C9
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 *
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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A; Residues: 1-935 <BAD>
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; Ng, W.V.; Kennedy,
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Cross-references: UNI
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;Species: Halobacterium sp. NRC-1
;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 2.1e+02;
1; Mismatches 2
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Pred. No. 1.8e+02;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1069 <PAG>
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                                     A; Molecule type: DNA
A; Residues: 1-223 <KJ
A; Cross-references: U
A; Note: the nucleotic
                                                                                                                                                                                    C;Accession: S76924
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; I DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobactes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ori, N.; Eshed, Y.; Paran, I.; Presting, G.; Aviv, D.; Tanksley, S.; Zamir, Plant Cell 9, 521-532, 1997
A;Title: The IZC family from the wilt disease resistance locus I2 belongs to targeterence number: Z15652, MUID:97290204; PMID:9144960
A;Accession: T06404
                                                                                                                               A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: confers resistance C;Superfamily: disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:076512; EMBL:AF074017; NID:g3328176; PIDN:AAC26789.1;
                                                                                                                                                                                                                                                                                                                                                               S76924
                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                              Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:024016; EMBL:AF004879; NID:g2258316; PIDN:AAB63275.1; PID:g2;
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;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                       Cross-references: UNIPROT: P74717;
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                                       the nucleotide sequence was
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Pred. No.
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Pred. No.
Score 27;
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                                                       EMBL: D90917;
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                                       GB:AB001339; NID:g1653836; PIDN:BAA1883 the EMBL Data Library, June 1996
                                                                                                                                                                                                                              T.; Watanabe, A.; Yamada,
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 Length 223;
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                 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
                                                                                R; anonymous,
Science 282,
                                                                                                                                                                      protein T07E3.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A;Residues: 1-224 <S
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A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH1019 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                     B88492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 176, 92-99, 1994
A;Title: An Azorhizobium caulinodans ORS571 locus involved in lipopolysaccharide
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;Species: Azorhizobium caulinodans
;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
                                                                                                                                ;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: UNIPROT:Q06936; EMBL:Z22611; NID:g296706; PIDN:CAA80331.1; PID:g2967;Superfamily: dTDP-dihydrostreptose synthase
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                                                                                                                             Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Accession: B88492
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                                                                                The C. elegans Sequencing Consortium 2012-2018, 1998
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Pred. No. 1.1e+02;
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  and www_sanger.ac.uk/Projects/C_ele, 1999; Science 283, 2103, 1999; and
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C;Accession: H83219

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, L.Dry, S.; Olson, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-312 <STO>
                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9HYI9;
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho;
A;Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                       A;Gene: PA3416
                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-333 <STO>
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A;Accession: H83219
                                                                                                                                                                                                                                                                                                                              Nature 406, 959-964, 2000
                                                                                                                                   ;Superfamily: pyruvate dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Species:
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                                                                  Matches
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004
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Pred. No.
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                                                                      Mismatches
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larity Conservat	2; AAB64703 ; S30862. 0978; ECM32 0978; ECM32 844; C:Doly 844; C:Doly 844; C:Doly 844; P:regu PR001410; D PR001410; D 1487; DEXDC; 1487; DEXDC; 1487; DEXDC; 1487; DEXDC; 1487; DEXDC; 1487; DEXDC; 1487; DEXDC; 1487; DEXDC;	SEQUENCE FROM N.A. STRAIN-S288C / AB972; STRAIN-S288C / AB972; MRDLINE-97313264; Pubm Dietrich F.S., Mulliga Araujo R., Aviles E., Cherry J.M., Chung E., Hyma Lin D., Mosedale D., N Oh C., Petel F.X., Rob Smith V., Taylor P., W "The nucleotide sequen Nature 387:78-81(1997) -I- SIMILARITY: Belong This SWISS-PROT entry between the Swiss Ins the European Bioinform use by non-profit i modified and this stat modified and this stat entities requires a li or send an email to li	STAN 31. 2 31. 3 31.	4444444444
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Micaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Strub M.L., Bleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P. Schrift T.
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Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacc Saccharomycetales; Saccharomycetaceae; Debaryomyces
                                              Transposase.
OrderedLocusNames=MM0258
                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CAG88524.1; -.
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001547; GlyCo_hydro_5.
SMART; SMO0382; AAA; 1.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
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1124 AA;
   Methanosarcinaceae; Methanosarcina
                  Archaea; Euryarchaeota;
                                Methanosarcina mazei (Methanosarcina frisia)
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STRAIN=CBS767;
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baryomyces hansenii chromosome B of strain CBS767
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                                                                                                                                                                                                                                       μ
                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                         LXXSLFERV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||||||
LETSLFERV 868
                                                                                                                                                                                                             LSLSLFERV 877
                                                                        (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       GLYCOSYL_HYDROL_F5; UNKNOWN_1.
                                                                                                                                                                                                                                                                                     91.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                127842 MW;
                                                                                                                                                                                                                                                                                  .88;
                                                                         222
                  Methanomicrobia; Methanosarcinales;
                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                    Score 31;
Pred. No.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                D6F8B09E58614EE9 CRC64;
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                                                                                                                                     378 AA
                                                                                                                                                                                                                                                                                    2e+02;
                                                                                                                                                                                                                                                                                                  DB 2;
                                                                           update)
                                                                                                                                                                                                                                                                                                  Length 1124;
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                                                                                                                                                                                                                                                                      Indels
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RESULT
Q6CDN7
  DT PRESENTATION OF THE PRE
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Best Local
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25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                             Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Gaffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Froy-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G. F., Straub M.L., Suleau A.,
Swemnene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Seniol-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE013250; AAM29954.1; -. GO; GO:0003577; F:DNA binding; IEA. GO; GO:0004803; F:transposase activity; IEA. GO; GO:0006313; P:DNA transposition; IEA. InterPro; IPR002559; Transposase_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yarrowia lipolytica ČLIB99.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22120827; PubMed=12125824;
Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R. Martinez-Arias R., Henne A., Wizer A., Baeumer S., Jacobi Brueggemann H., Lienard T., Christmann A., Boemecke M., Ste Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gun Fritz H.-J., Gottschalk G.;
ORFNames=YALIOB22528g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transfer between Bacteria and Archaea. To Mol. Microbiol. Biotechnol. 4:453-46.
                                                                                                                                    STRAIN=CLIB99
                                                                                                                                                                                                                  Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                   Bouchier C., Caudron B., Scarpelli C., Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yarrowia lipolytica
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"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ipolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO1 / ATCC BAA-199 / DSM 3647 / OCM
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; I
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4:453-461(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   867
                                                    protein kinase family.
                                                                                                                                                                                                                                                                                               Gaillardin C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Yarrowia
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                                                                                                                                                                                                                                                                                                  Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Daruvar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunsalus
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
B Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Micaud J.M., Nikolski M., Oztas S., Ozier Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Witth B.,
Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Michar P., Souciet J.L.;
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Best Local S
Matches 6
                                                                                                                            Query Match
Best Local
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Pfam; PF000069; Pkinase; I.

ProDom; pD000001; Prot kinase; 1.

SMART; SM00220; S TKG; I.

SMART; SM00220; TYrKG; 1.

SMART; SM000219; TYrKG; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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Q6FKF3;
Q6FKF3;
Q6FKF3;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q6FKF3;
Q6F
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InterPro; IPR000719; Prott kinase.
InterPro; IPR002290; Ser_thr pkinase.
InterPro; IPR008271; Ser_thr pkin_AS.
InterPro; IPR008271; Tyr_pkinase.
Pfam; PF00069; Pkinase; 1.
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                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                         "Genome evolution in yeasts.";
Nature 430:35-44(2004).
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Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genolevures;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=284593;
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GO:0006468;
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865
                                                                                                                                                                                                         CR380958; CAG62265.1;
NCE 1125 AA; 127137
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                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LXXSLFERV
                                                    LXXSLFERV 9
LSLSLPERI 873
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:protein serine/threonine kinase activity; F:protein-tyrosine kinase activity; IEA.
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                                                                                                                            88.2%;
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                                                                                                      Score 30; DB
Pred. No. 3.5e
1; Mismatches
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                  63C0428123F3CC8C
                                                                                           DB 2;
3.5e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                          Length 1125;
                                                                                                                                                                                                                  CRC64;
                                                                                                         Indels
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RESULT

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RESULT 7
Q8PSN2
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                            Q8PSN2;
Q8PSN2;
01-OCT-2002
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8PRQ1;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01609; Transposase_11;
Complete proteome.
SEQUENCE 378 AA; 43945 MW;
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EMBL; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R. Fritz H.-J., Gottschalk G.;
                                                      Pritz H.-J., Gottschalk G.;
"The genome of Methanosarcina mazel: evidence for transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
                                                                                                         Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Stecke Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsal
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EMBL; AE013560; AAM32743.1; -. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0004803; F:transposase activity; GO; GO:0006313; P:DNA transposition; IEA
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE=22120827; PubMed=12125824;
                                                                                                                                                                                                                                                     Methanosarcina mazei (Methanosarcina fris
Archaea; Euryarchaeota; Methanomicrobia;
                                                                                                                                                                                                                                                                                                 Transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB013494; AAM32203.1; -.
EMBL; AB013585; AAM32961.1; -.
EMBL; AB013585; AAM32965.1; -.
EMBL; GO:0003677; F:DNA binding; IEA.
GO; GO:0004803; F:transposase activity;
GO; GO:0006313; P:DNA transposition; IEA.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanosarcina mazei (Methanosarcina fris
Archaea; Euryarchaeota; Methanomicrobia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transposase
                                                                                                                                                                                                                                          Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                    OrderedLocusNames=MM3047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
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"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22120827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                           159
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                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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827; PubMed=12125824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.3%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Last annotation updat
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Pred. No. 2.1e+02;
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                IEA.
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                                                                                                                                                                                                                                                          Methanosarcinales;
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                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 378;
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                                                                                    lateral gene
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                                                                                                                  Gunsalus
                                                                                                                               Steckel S.
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RESULTATION OF THE PROPERTY OF
RESULT 9
Q7MHH8
ID Q7MH
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AC Q7MH
DT 01-M
DT 01-
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPKVVVII InterPro; IPKVVVII InterPro; IPKVVVII InterPro; IPKVVVII I.
Pfam; PP00679; EFG_TV; 1.
Pfam; PP00764; EFG_TV; 1.
TIGRFAMS; TIGR00231; small GTP; 1.
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Best Local
                                                                                                                                                                                                                        Q7MHH8;
Q7MHH8;
01-MAR-2004
01-MAR-2004
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Q7YYP3;
01-OCT-2003
                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein VV2891.
OrderedLocusNames=VV2891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BX538352; CAD98437.1; -.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003746; F:translation elongation factor
   NCBI_TaxID=196600;
                                    Vibrionaceae; Vibrio.
                                                               Bacteria; Proteobacteria;
                                                                                                Vibrio vulnificus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptosporidium parvum."; Genome Res. 0:0-0(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bankier A.T., Spriggs H.F., Fartmann B., Kon
Vogel C., Teichmann S.A., Ivens A., Dear P.I
"Integrated mapping, chromosomal sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cryptosporidium parvum.
Bukaryota; Alveolata; Apicomplexa;
Cryptosporidiidae; Cryptosporidium.
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
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Pfam; PF01609; Transposase_11; 1.
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InterPro; IPR005517; EFG_IV.
InterPro; IPR005517; EFG_IV.
InterPro; IPR005225; Small_GTP.
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                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                               Gammaproteobacteria; Vibrionales;
                                                                                                    YJ016)
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Pred. No. 5.9e
1; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                            PRT;
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Protein biosynthesis.
8E01582248B66F83 CRC
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STRAIN-GSS1 / DSM 4299 / JCM 9571;

STRAIN-GSS1 / DSM 4299 / JCM 9571;

X MEDLINE-20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;

XA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

XA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

XA Kawashima T., Amano N., Koike H., Makino K., Suzuki M.;

XI Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

XI "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";

Sequ
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
Probable cobalt-precorrin-6Y C(15)-methyltransferase [decarboxylating]
(EC 2.1.1.-)
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PubMed=14659965; DOI=10.1101/gr.1295503;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermoplasma yolcanium. Archaea; Euryarchaeota; Thermoplasmataceae; Ther
                                                                    HAMAP; MF_00786; -; 1.
InterPro; IPR000051; SAN
Cobalamin biosynthesis;
                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q97A64;
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       SEQUENCE
                                      Transferase.
                                                                                                                                                                                      EMBL; AP000994; BAB60088.1; -.
                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          corrin ring synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=cbiT; OrderedLocusNames=TV0946; ORFNames=TVG0972073;
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EMBL; AP005341; BAC95655.1; -.
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InterPro; IPR000515; BPD transp.

InterPro; IPR010065; HEQRO_ABC_3TM.
Pfam; PF00528; BPD transp. 1; 1.

TIGNPAMB; TIGR01726; HEQRO_perm_3TM; 1.
PROSITE; PS50928; ABC_TM1; 1.

Complete proteome; Transmembrane; Transpore.
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Q6F7F6;
05-JUL-2004;
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05-JUL-2004;
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Blover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.B.W., Lory S., Olson M.V.,

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:595-964 (2000).

-I-FUNCTION: Part of a binding-protein-dependent transport system.

Probably responsible for the translocation of the substrate across
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Q916H8;
01-MAR-2001
                               Hypothetical protein.
OrderedLocueNames+ACIAD3340;
Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
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MEDLINE=20437337;
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01-MAR-2004 (TrEMBLrel.
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SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
SIMILARITY: Belongs to the binding-protein-dependent transport
System permease family.
L; AB004469; AAG03702.1; -.
L; H83606; H83606.
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Last annotation update)
                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 2.3e
1; Mismatches
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RESULT 13
Q8UDZ2
ID Q8UDZ
COUDEZ; Q7CY60;

T 01-UN-2002 (TRRBLrel. 21, Created)

T 01-UN-2002 (TRRBLrel. 21, Last sequence update)

T 01-UN-2002 (TRRBLrel. 22, Last annotation update)

T 25-QCT-2004 (TRRBLrel. 28, Last annotation update)

S Cyclopropane-fatty-acyl-phospholipid synthase (AGR_C_3:

N Name=cfa; OrderedLocusNames=AGR_C 3595; Atu1974;

N Name=cfa; OrderedLocusNames=AGR_C 3597).

OS Agrobacterium tumefaciens (straIn_C58 / ATCC 33970).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobi

CR Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacte
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Best Local S
Matches 6
                           MEDLINE-21608551; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Bpp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                        wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labarre L., Cruvelller S., Robert C., Duprat S., Wincker P., Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; "Unique features revealed by the genome sequence of Acinetobacter sp. ADP1, a versatile and naturally transformation competent bacterium."; Mucleic Acids Res. 0:0-0(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Dupont;
MEDLINE=21608550;
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PROSITE; PS50263; CN HYDROLASE; 1.
PROSITE; PS01227; UPF0012; UNKNOWN_1.
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GO; GO:0016810; F:hydrolase activity, a
GO; GO:0006807; F:nitrogen metabolism;
InterPro; IPR003010; Ntlse/CWhydtse.
InterPro; IPR001110; UPP0012.
                                                                                                                                                                                                                                                                                                               Nester E.W.;
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                                                                                                                                                                                                                                                                                           of the natural genetic engineer Agrobacterium tumefaciens
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|llarity 100.0%;
|Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11743193; DOI=10.1126/science.1066804;
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Pred. No.
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Dolan M.,
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RESULT 14
Q7VUF
ID Q7VUF
AC WANTEF
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RESULT 15
Q95UP7
ID Q95UP
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DT 01-DE
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Best Local
                   Q95UP7;
Q95UP7;
01-DEC-2001
01-DEC-2001
01-JUN-2003
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PIR; D97597; D97597.
GO; GO:0008825; F:cyc
GO; GO:0008610; P:lip
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Q7VJP0;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
UDP-galactopyranose mutase (EC 5.4.99.9).
Name=glf; OrderedLocusNames=HH0203;
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MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell' M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
Potassium inwardly rectifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017144; AAP76800.1;
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Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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SEQUENCE 341 AA; 39042 MW;
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         (TremBLrel. 19, Created)
(TremBLrel. 19, Last sequence update)
(TremBLrel. 24, Last annotation update)
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66.7%; Pred. No. 3.6e+02;
tive 1; Mismatches 2
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GO; GO:0005242; F:inward rectifier potassium channel activity;
GO; GO:000527; F:potassium channel activity; IEA.
GO; GO:0005244; F:voltage-gated ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22126605; PubMed=12128223; DOI=10.1016/S0925-4773(02)00140-5; MacLean S.J., Andrews B.C., Verheyen E.M.; "Characterization of Dir: a putative potassium inward rectifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                            Ion transport; Ionic channel; Potassium; Potassium transport;
Transmembrane; Transport; Voltage-gated channel.
SEQUENCE 422 AA; 48457 MW; 40AC1956E9B29C3B CRC64;
                                                                                                                                                                            PRINTS; PR01320; KIRCHANNEL.
                                                                                                                                                                                         Pfam; PF01007; IRK; 1.
                                                                                                                                                                                                        InterPro; IPR001838; K+channel_IR.
InterPro; IPR001622; K+channel_pore.
                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0039061; Ir.
                                                                                                                                                                                                                                                                                                                                                     HSSP; P35562; 1N9P
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY044166; AAK98804.1; -.

    -!- SUBCELLULAR LOCATION: Integral membrane protein (
    -!- SIMILARITY: Belongs to the inward rectifier-type

                                                                                                                                                                                                                                                                                                                                                                                                                                   Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                    family.
 374
                               н
                                                             Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 in Drosophila.";
ev. 116:193-197(2002)
| |||:|:
|SASLFQRI
                                 LXXSLFERV 9
                                                                Conservative
 382
                                                                             82.4%;
                                                                2;
                                                                             Score 28; DB 2;
Pred. No. 4.1e+02;
                                                                Mismatches
                                                                                              Length 422;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).

potassium channel
                                                                0
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                                                                Gaps
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Search completed: April 18, 2005, 08:15:45 Job time : 39.5766 secs

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Res
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
:
                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                           US-10-652-334-6
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              April 18, 2005, 07:10:15; Search time 104.54 Seconds (without alignments) 77.692 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2105692 segs, 386760381 residues
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqp2000s:*
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                                                                      SUMMARIES
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No.	Score	Query	Length	ВB	ID	
۲	78	86.7	21	7	ABW01182	Abw01182 Saccharom
N	78		21	8	ADP44108	۲ 8
ω	78	86.7	22	w	AAY77809	Motif V
4.	7	•	415	w	AAY77813	Yeast
₅	67.5	75.0	415	7	ABW01201	Abw01201 Saccharom
0	67.5	•	415	æ	ADP44127	7
7	65.5	72.8	925	œ	ADN19434	Adn19434 Bacterial
œ	65.5	72.8	992	8	ADS23757	-
9	64.5	71.7	471	w	AAY77815	Aay77815 Yeast Sen
10	64.5	71.7	472	7	ABW01202	Abw01202 Saccharom
1	64.5	71.7	472	8	ADP44128	Adp44128 Yeast hel
12		71.7	2000	σ	ABR53451	Abr53451 Protein s
13	•	71.7	2000	7	ADK64622	Adk64622 Disease t
14	64.5	71.7	2231	œ	ADN19177	Adn19177 Bacterial
15	61.5	68.3	71	8	AB058160	Abo58160 Human gen
16		68.3	797	N	AAW36508	Aaw36508 Human REN
17	61.5		935	7	ADJ69900	Adj69900 Human hea
18	61.5	68.3	1043	N	AAW36509	Aaw36509 Murine RE
19			1118	σ	ABG73900	Abg73900 Human REN
20			1140	N	AAY21377	Human
21			380	w	AAY77814	Aay77814 Yeast Upf
22			380	7	ABW01205	Saccha
23		66.1	380	8	ADP44131	Adp44131 Yeast hel
24	59.5	66.1	642	œ	ADS43096	Ads43096 Bacterial
25		66.1	818	œ	ADK68058	Adk68058 Female re

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3 AAY98057 Aay98057 ABR53312 ADX64706 ADX64706 ADX643706 ADM25464 ADM19968 ADM19968 ADS44332 AAM39674 AAM39677 AAB52377 ADR58327 AAM52318 AAM41460 AAM41460 AAM41460 AAM79295 AAM41460 AAM79295 AAM71816 AAM791816 AAM791816 AAM791816 AAM777816 AAD944130 BAD944130 ADS43834 AAM94130 Ad843834	52.8	52.8	. 52.8	52.8	53.3	56.7	57.8	. 57.8	57.8	57.8	57.8	57.8	57.8	57.8	57.8	58.9	59.4	66.1	66.1	66.1
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reast Upf Protein s Disease t Hyperther Sacterial Sacterial Human pol Human pro NM 015046 PRÖ polyp Human pol		_	_		_	-				-		_	-			_				-
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ALIGNMENTS

ABW01182 standard; peptide; 21

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RESULT 1
ABW011820
ID ABW0
XX ABW0
XX ABW0
XX ABW0
XX First Sacc
XX Modu
XW thet
XX Modu
XW th ABW01182; Saccharomyces cerevisiae. Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast. Saccharomyces cerevisiae motif VI peptide 15-JAN-2004 (first entry)

/label= Unknown /note= "Xaa may Misc-difference 10 07-OCT-2003. Misc-difference Peltz S, Czaplinski K, 22-JUL-1999; US6630294-B1. Misc-difference Misc-difference Misc-difference (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY. 22-JUL-1998; Misc-difference 98US-0093685P. 99US-00359268. Location/Qualifiers /label= Unknown /note= "Xaa may be any amino acid" /label= Unknown /note= "Xaa may be any /note= "Xaa may 'label= Unknown 'note= "Xaa may /label= Unknown /note= "Xaa may label= Unknown Dinman JD; be any be any be any be any amino acid" amino acid" amino acid" amino acid" amino acid"

WPI; 2003-810549/76.

Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific

Disclosure; Col 43-44; Opp; English

binding

to Mtt1.

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RESULT 2
ADP44108
ADP44108
ADP44108
ADP44108
AC ADP4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Von Willebrand Disease; Osteogenesis Imperfecta; Breast Cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinits Bigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; buchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B;
                          (PELT/)
(CZAP/)
                                                                                                     22-JUL-1998;
22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2004
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                                                                                                                                                                               28-AUG-2003; 2003US-00652334.
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  (DINM/)
                          PELTZ S.
CZAPLINSKI K.
  DINMAN J D.
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99US-00359268.
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Pred. No.
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the RNA helicase MTTI with a composition or agent under conditions
CC permitting binding between the MTTI and the composition, detecting
CC specific binding of the test composition or agent to the MTTI. The
CC composition and methods are useful for modulating the fidelity of
CC translation termination or for identifying agents that: affect the
CC translation activity of mRNAs by altering frameshift frequency, permit
CC transcripts, and provide modulators (inhibitors/stimmation of aberrant
CC transferase activity during initiation, elongation, termination and mRNA
CC degradation of translation. The agents, which may be antagonists or
CC gonists, are useful in screening, disgnostic and therapeutic purposes,
CC for diseases or conditions resulting from or cause premature translation,
CC such as beta-thalassaemia, beta-globin, Duchemne/Becker Muscular
CC Dystrophy, Haemophilia A, Haemophilia B, Von Willebrand Disease,
CC Osteogenesis Imperfecta, Breast cancer, Ovarian Cancer, Wilms Tumour,
CC Hirschsprung disease, Cystic fibrosis, Kidney Stones, Familial
CC hypercholesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis,
CC the amino acid sequence of the yeast translation termination modulation
CC protein motif vr
Identifying a test composition or agent that modulates the efficiency translation termination comprises contacting the MTTI with the test composition or agent, and determining if the test composition or agent inhibits the MTTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Czaplinski K,
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RRESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LXXQYRMHPXISEFPXYXGXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LXXQYRMHPXISEFPXYXGXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Helicase B; HCSB; MTT1; modulator of translation termination; eRF1 eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.

eRF1; eRF3;

Motif VI comprised in a gene modulating translation termination

22-JUL-1999; 03-FEB-2000.

99WO-US016802.

WO200005586-A2

Misc-difference

Location/Qualifiers

/note= "reisdues indicated Xaa are unspecified"

Unidentified.

31-MAY-2000

(first entry)

δ

Sequence 21

Ā

protein motif VI.

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RESULT 4
AAY/7181
ID AAY/7
XX
AC AAY/7
XX
DT 31-V
DT 31-V
DE Yeas
XX
V
EXW Hell
XW Hell
XW bett
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC transferase activity, especially diseases resulting from a nonsense or CC frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker CC Muscular Dystrophy etc. It can be used to identify disease conditions CC involving a defect in the complex, by transfecting cells with encoding CC nucleic acid and determining the proportion of defective complex before and after transferase activity during translation, inhibiting the peptidyl transferase activity during translation, inhibiting the CC interaction between MTI and eRR3 or involved in enhancing translation termination. Vectors comprising polynucleotides encoding the complex (or contisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of cranslation termination of mRNA and/or degradation of aberrant CC transcripts in a cell. Agents binding to the complex can be identified can included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation of aberrant CC transcripts in cells. The method can be useful to identify agents of compositions modulating binding to MTTI, useful to identify genes.

CC sequences AAY77804-812 represent motifs I-IX comprised in the genes of othersers usef for modulating translation to reministion the genes of othersers usef for modulating translation to identify genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                      Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                        Saccharomyces cerevisiae
                                                                                                                                                                                      Yeast Mttl protein fragment
                                                                                                                                                                                                                                        31-MAY-2000
                                                                                                                                                                                                                                                                                                                                 AAY77813 standard; peptide; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidyl transferase activity during translation.
the gene encoding Helicase B (HCSB; renamed MTT1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 38; Page 79; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-171458/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LXXQYRMHPXISEFPXYXGXL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LXXQYRMHPXISEFPXYXGXL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used
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                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provides a new multiprotein complex which can modulate
sferase activity during translation. The complex comprises
ding Helicase B (HCSB; renamed MTT1, for Modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00120435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dinman JD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          eRF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i
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ABW01201
ID ABW
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                                                                                                                                                                                              RESULT 5
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                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               termination. Vectors comprising polynucleotides encoding the complex (or antisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation of aberrant transcripts in cells. The method can be used to identify agents/
compositions modulating binding to MTT1, useful to identify agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved i peptidyl transferase activity during translation, inhabiting the interaction between MTT1 and eRF3 or involved in chancing translation interaction between MTT1 and eRF3 or involved.
                                                                          15-JAN-2004
                                                                                                                 ABW01201;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRP) 1 and eRP3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in
                                                                                                                                                       ABW01201 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAY77813-817 represent protein fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidyl transferase activity during translation. The complex comp
the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of
Translation Termination) and the conserved proteins known to inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200005586-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-171458/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNE-) UNIV NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                    213
                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                         1 LXXQYRMHPXISEFP---XXXGXL 21
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                    LDTQYRMHPKISEFPIKKIYNGEL 236
                                                                                                                                                                                                                                                                                                                                                                                                              415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity e.g.
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         provides a new multiprotein complex which can modulate sferase activity during translation. The complex comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00120435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US016802
                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dinman
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                 Score 67.5; DB 3;
Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                          ω
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                                                                                                                                                                                                                                                                                                                                                                    Length 415;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identify genes.
from yeast superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to interact and
                                                                                                                                                                                                                                                                                                                                 ω
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                                                                                                                                                                                                                                                                                                                                 Gaps
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Modulator of translation termination; MTT1; helicase B; antiviral; Saccharomyces cerevisiae modulator of translation termination protein.

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ADP44127 6
ADP427 ID ADP4
XX ADP4
XX ADP4
XX ADP4
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX Hran
XW Pepp
XW Von
XW Ovar
XW Neur
XX Ne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia, beta-globin; peptidyl transferase modulation; beta-thalassaemia, beta-globin; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B Duchenne/Becker Muscular Dystrophy; Haemophilia B; Cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Wilms Tumour; Hirschsprung disease; Cystic fibro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae MTT1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-2003.
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22-JUL-1998;
22-JUL-1999;
                                                                                      28-AUG-2003;
                                                                                                                                                 17-JUN-2004
                                                                                                                                                                                                           US2004115787-A1
                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                              Neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast helicase Mttl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP44127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP44127 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 49-52; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-810549/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15,
                                                                                                                                                                                                                                                                                                                                                          1 Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LXXQYRMHPXISEFP---XYXGXL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to Mttl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDTOYRMHPKISEFPIKKIYNGEL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿,
                                                                                      2003US-00652334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation termination; RNA helicase; MTT1;
98US-0093685P.
99US-00359268.
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                                                                                                                                                                                                                                                                                                                              Retinoblastoma; ATM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67.5; DB 7;
Pred. No. 0.00054;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                 Costmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                 Disease;
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                                                                                                                                                                                                                                                                                                                                 yeast; enzyme.
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the RNA helicase MTT1 with a composition or agent under conditions
CC permitting binding between the MTT1 and the composition, detecting
CC specific binding of the test composition or agent under conditions
CC determining if the test composition or agent inhibits the MTT1, and
CC composition and methods are useful for modulating the fidelity of
CC translation termination or for identifying agents that: affect the
CC functional activity of mRNAs by altering frameshift frequency, permit
CC transcripts, and provide modulators (inhibitors/stimulators) of peptidyl
CC transferase activity during initiation, elongation, termination and mRNA
CC degradation of translation. The agents which may be antagonists or
CC agonists, are useful in screening, diagnostic and therapeutic purposes,
CC of diseases or conditions resulting from or cause premature translation,
CC such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscullar
CC Osteogenesis Imperfecta, Breast cancer, Ovarian Cancer, Wilms Tumour,
CC Hirschaprung disease, Cystic fibrosis, Kidney Stones, Pamilial
CC Hypercholesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis,
CC Retinoblastoma, ATM or Costmann Disease. The present sequence represents

CC the amino acid sequence of the yeast helicase Mtt1.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-449400/42
                                                                                                                                                                                                                                         Bacterial polypeptide #2087.
                                                                                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                                                                                            ADN19434 standard; protein; 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of identitying a t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peltz S,
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                                                                                                      bacterial
                                                                                                                        nitrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibits the MTT1
                                                                                                                                                                                                                                                                                                                                                                                                                                 213 LDTQYRMHPKISEFPIKKIYNGEL 236
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CZAPLINSKI K.
DINMAN J D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LXXQYRMHPXISEFP---XYXGXL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 AA;
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                                                                                                    phosphorus; photosynthesis; lignin;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to a method of identifying a test composition that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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18-DEC-2003

US2003233675-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC content, improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part form in the printed specification but was obtained in electronic condition.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                         Bacterial polypeptide #12790.
                                                                                                                                                                                                  ADS23757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                 02-DEC-2004
                                                                                                                                                                                                                                    ADS23757 standard; protein; 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2087; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant DNA construct comprising
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SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at seqdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                   72.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                Score 65.5; DB 8
Pred. No. 0.0033;
1; Mismatches
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RESULT
AAY7781
ID AA
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AC AA
AC AA
XX
AC AA
XX
YX
YX
YY
DE ^Yee

AAY77815 standard;

peptide; 471

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31-MAY-2000 AAY77815;

(first entry)

Yeast Senl protein fragment.

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                                                                                                                                                 CC promoter functional in a plant cell, where the promoter is positioned to comprising the recombinant DNA construct and a method of producing a crop plant cell. CC comprising the recombinant DNA construct and a method of producing a crop plant cC transformed plant having an improved property. The plant is a crop plant cC such as maize or soybean. The method of producing a transformed plant cC having an improved property comprises transformed plant cC having an improved property comprises transforming a plant with the crop plant DNA construct and growing the transformed plant, where the cC polymucleotide or polypeptide is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, concreased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate growth rate of homologous recombination, modified seed oil or protein yield and/or cC content, improved yield by modification of carbohydrate, nitrogen or cphosphorus use and/or uptake, by modification of carbohydrate, nitrogen or content, improved plant growth and development under at least one stress condition, improved lighin production of carbohydrate, nitrogen or conduction. This sequence erepresents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not corm part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                       Matches
                                                                                                         Query Match
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 12790; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-061375/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAOY/)
                                                                                          Local
 566
                                   1 LXXQYRMHPXISEFPX---YXGXL 21
                                                                     l Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinkle GJ,
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SLATER S
CHEN X.
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LNVQYRMHPCLSEFPSNMFYEGSL 589
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58.3%;
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                                                                     Score 65.5; DB 8
Pred. No. 0.0036;
1; Mismatches
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                                                                                                           DB 8;
                                                                                                       Length 992;
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RESULT 10
ABW01202
ID ABW01
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                                                                                                                                                                                                                                                                                                 cc peptidyl transferase activity during translation, inhibiting the complex comprising polynucleotides encoding the complex comprising polynucleotides encoding the complex (or contrasters enquences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of transcripts in a cell. Agents binding to the complex can be identified concluded in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They care also useful to modulate the efficiency of transcripts in cells. The method can be used to identify agents/c compositions modulating binding to MTT1, useful to identify agents/c compositions modulating binding to MTT1, useful to identify agents/c repoint 1 helicases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl celkaryotic release factor (eRF) l and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transferting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved in
                                                                                                                                                                          Matches
                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
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                                                                                                                                                                                                                                                  Sequence 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a new multiprotein complex which can modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNE-) UNIV NEW JERSEY
                                                                                                300
                                                                                                                                                                          14; Conservative
                                                                                                                                                                                            Similarity
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                                                                                                                                    LXXQYRMHPXISEFPX---YXGXL 21
                                                                                              LDVQYRMHPSISKFPSSEFYQGRL 323
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                                                                                                                                                                                          71.7%;
58.3%;
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                                                                                                                                                                        Score 64.5; DB 3
Pred. No. 0.0023;
1; Mismatches
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ABW01202 standard; protein; 472 AA

Saccharomyces cerevisiae

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RESULT 11
ADP44128
ID ADP444
XX ADP44
XX ADP44
XX ADP44
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XX Yeast
XX Yeast
XX Yeast
XX Yene
KW Gene
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                                            gene therapy; translation termination; RNA helicase; MTT1; frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast; enzy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae SEN1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mtt1) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
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                                                                                                                                                                                                                                                                                     ADP44128 standard; protein; 472 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2004 (first entry)
                                                                                                                                                                                            Yeast helicase Senl.
                                                                                                                                                                                                                          18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding to Mtt1.
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14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                          (first entry)
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Pred. No. 0.
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RESULT 12
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a test composition or agent that modulates the efficiency translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent inhibits the MTT1.
BP1258494-A1
                           Saccharomyces cerevisiae
                                                         Multiprotein
                                                                                      Protein sequence
                                                                                                                    20-JUN-2003
                                                                                                                                                 ABR53451;
                                                                                                                                                                          ABR53451 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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22-JUL-1999;
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DINMAN J D.
                                                                                                                                                                                                                                                     LDVQYRMHPSISKFPSSEFYQGRL 324
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                                                         complex; eukaryote;
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58.3%;
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Pred. No. 0.00
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                                                       drug target; diagnosis.
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RESULT 13
ADK64622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bauer A,
Marzioch
Bauer A, Gavin A,
Marzioch M, Grandi
Michon A, Leutwein
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                                                                                                                                                                                                                                                                    27-AUG-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  protein complex; drug target; diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     document is available on CD-ROM
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M, Schultz
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G
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Superti-Furga G, Kue
P, Krause R, Kruse
C, Rick J;
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58.3%;
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Superti-Furga GD;
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                                                          Schultz J;
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PD 18-DE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homelogue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that
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N-PSDB; ADK64623.
(HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                          18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial polypeptide #1830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2127; 13pp; English.
                                                                                                21-FEB-2002; 2002US-0360039P
                                                                                                                                   20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                              US2003233675-A1
                                                                                                                                                                                                                                                                                                        nitrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN19177 standard; protein; 2231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2000 AA;
                                                          (CAOY/)
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HINKLE G
SLATER S
CHEN X.
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                                                          CAO
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                                                                                                                                                                                                                                                                                       phosphorus;
polypeptide
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                       n q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%;
58.3%;
                                                                                                                                                                                                                                                                                                        photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64.5; DB 7;
Pred. No. 0.013;
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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a CC comprising the recombinant DNA construct and a method of producing a crop plant cc such as maize or sybean. The method of producing a transformed plant cc such as maize or sybean. The method of producing a transformed plant cc having an improved property comprises transforming a plant with the crecombinant DNA construct and growing the transformed plant, where the cc polynucleotide or polypeptide is useful for improving plant properties. CC intercombinant DNA construct is useful for producing plants with the recombinant DNA construct is useful for producing plants with the cc inproved plant properties, e.g. improved cold, heat or drought tolerance, comprises transformed plant, where the cc increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate by modification of the cell cycle pathway with plant growth rate by modification or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by production, improved lignin production or improved galactomannan cc condition, improved lignin production or improved galactomannan cc condition. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic cc format from USPFO at sequence data for this patent did not compare the printed specification but was obtained in electronic cc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                               03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                   Human; gene
alternative
                                                                                                                                                                                                                                                                                                         Human genome derived single exon protein #4394.
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                                                       03-APR-2002; 2002US-00029386
                                                                                                                                  16-OCT-2003
                                                                                                                                                                          US2003194704-A1
                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1830; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
14; Conserv
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                                                                                                                                                                                                                                                   expression; single exon probe; microarray; splicing event; genomic alteration.
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
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Job time: 104.651 secs
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                                                                                                                                                                                                                                                                                                                              contiguous amino acids of any of the above, an one-contiguous amino acids of any of the above-mentioned amino acid so fany of the above-mentioned amino acid conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing to measure gene expression, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising smaller genomic alterations, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human can be succeed in electronic format directly from USPTO at sequence in electronic format directly from USPTO at sequence.html?Doc1D=20030194704
                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                             Sequence 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 45;
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                                                                                                                                                1 LXXQYRMHPXISBFPX---YXGXL 21
                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                          Score 61.5; DB 8; Length 71; Pred. No. 0.00093; Indels 1; Mismatches 7; Indels
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US-09-39-268A-29
US-09-39-268A-28
US-09-39-35-268A-8
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US-09-370-767-8804
US-09-270-767-8804
US-09-270-767-8804
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US-09-248-796A-19347
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APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
TITLE OF INVENTION: A SUBPAMILY OF RNA HELIC
TITLE OF INVENTION: THE FIDELITY OF TRANSLAT
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
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                                                                                                                                  Sequence 25, Application Patent No. 6630294 GENERAL INFORMATION:
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.
19126, A	16127, A	6904, Ap	52, Appl	•	48, Appl	46, Appl	44, Appl	21, Appl	11, Appl	8, Appli	5, Appli	3, Appli	3, Appli	3, Appli	6, Appli	1, Appli	5447867

ALIGNMENTS

APPLICANT: Peltz, Stuart APPLICANT: Czaplinski, Kevin APPLICANT: Dinman, Jonathan D. APPLICANT: Dinman, Jonathan D. TITLE OF INVENTION: A SUBPANILY OF RNA HELIC TITLE OF INVENTION: THE FIDELITY OF TRANSLAT TITLE OF INVENTION: THEREOP FILE REFERENCE: 601-1-85N CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT APPLICATION NUMBER: 00/093,685 PRIOR FILING DATE: 1998-07-22 PRIOR PILING DATE: 1998-07-22 UNMBER OF SEO ID NOS: 32 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6 LENGTH: 21 TYPE: PRT ORGANISM: Saccharomyces Carevisiae FEATURE: OTHER INFORMATION: Xaa = US-09-359-268A-6 RESULT 1 US-09-359-268A-6 GENERAL INFORMATION: Sequence 6, Application US/09359268A Patent No. 6630294 Matches Query Match Best Local Similarity ORGANISM: Saccharomyces cerevisiae . 1 LXXQYRMHPXISBFPXYXGXL 21 21; Conservative LXXQYRMHPXISEFPXYXGXL A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES 86.7%; any amino 0; Score 78; Pred. No. 21 Mismatches acid 1.08 .2e-07 4 0 Length 21; Indels <u>.</u> Gaps 0

US/09359268A

RNA HELICASES WHICH ARE MODULATORS F TRANSLATION TERMINATION AND USES

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                                                            US-09-248-796A-18134
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LENGTH: 917
TYPE: PRT
                                                                                                                                PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18134
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
Best Local Similarity
                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18134, Application US/09248796A Patent No. 6747137
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                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 199-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICÁN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                  TYPE: PRT
                                                                              ORGANISM: Candida albicans
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                                                                                                                ENGTH:
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62.5%;
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62.5%;
72.8%;
58.3%;
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Pred. No. 0.00059;
0; Mismatches 6
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Pred. No. 0.00025;
Score 65.5; DB 4; Pred. No. 0.00013;
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                  Length 106;
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US-08-724-354D-4
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Sequence 4, App...
No. 5994119
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Patent No. 663029
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29 APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         ATERT NO. 377....GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
APPLICANT: MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: SOFTWARE: Patentin V
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                                                                                                                                                                                                                                                  ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                 STREET: 4225 E
CITY: La Jolla
                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                     STATE:
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Suite 1400
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RESULT 8
US-08-724-354D-2
; Sequence 2, Application US/08724354D
; Patent No. 5994119
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1043 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haile, Liea A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM:
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                                                                                                 621 LQVQYRMHPALSAFPSNIFYEGSL 644
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                                                                                                                                                          13,
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                                                                                                                           1 LXXQYRMHPXISEFPX---YXGXL 21
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                            linear
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                                                                                                                                                                      68.3%;
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54.2%;
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                                                                                                                                                       Pred. No. 0.0084;
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                                                                                                                                                                                      DB 3; Length 1043;
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US-09-270-984A-2
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Applic
Patent No. 6048965
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1118 amino aci
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APPLICANT: Dietz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0756
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                      COMPUTER: IBM Compatible
OPERATING.875TEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/724,:
FILING DATE: 01-OCT-196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      CITY: La Jolla
STATE: CA
                                                                                                                                                                                   ZIP: 92037
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OPERATING SYSTEM:
                                                     APPLICATION NUMBER:
                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson, ADDRESSEE: 4225 Excutive Square, Suite 1400
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                                                       US/09/270,984A
   08/724,354
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Pred. No. 0.0091;
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US-09-359-268A-29
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                                                                         APPLICANT: Peltz, Stu
APPLICANT: Czaplinoki
APPLICANT: Dinman, Jo
TITLE OF INVENTION: A
TITLE OF INVENTION: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10116
                                                                                                                                                                                             Sequence 29, Application US/09359268A Patent No. 6630294
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Best Local Similarity
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SENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OP INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OP INVENTION: WITH HUMAN DISEASE, METHODS
PILE REPERENCE: CL001307
FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1140
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                  720 LQVQYRMHPALSAFPSNIFYEGSL 743
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                                                                                                                                    Czaplinski, Kevin
                                                                                                                                                         Peltz, Stuart
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                                                                             A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES
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54.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.5; DB 4; Length 1140; Pred. No. 0.0093;
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OF DETECTION AND USES THEREOF
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US-08-724-354D-22
; Sequence 22, Application US/08724354D
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                                                               Query Match 66.1%;
Best Local Similarity 54.2%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
                                                                                                                                                                                                                                     TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
OPERATE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                 NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 077
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92037
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                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                      LENGTH:
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 634 LEVOYRMNPYLSEPPSNMFYEGSL 657
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                               1 LXXQYRMHPXISEFPX---YXGXL 21
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4225 Excutive Square, Suite 1400
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54.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/093,685
                                                                                                                                                                                                                                                                                                        07265/090001
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Pred. No. 0.0065;
                                                                Score 59.5; DB
Pred. No. 0.018;
2; Mismatches
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RESULT 13 US-09-270-984A-22 ; Sequence 22, Application US/09270984A

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Patent No. 6048965

GENERAL INFORMATION:

APPLICANT: Dietz, Harry C. TITLE OF INVENTION: MAMMALIAN REGULATOR OF TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY

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RESULT 14
US-09-177-431-8
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Patent No. 6071700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.1%;
Best Local Similarity 54.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
                                                                                                                                                                                                                                                   APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                   TITLE OF INVENTION: HETEROLOGOUS PO
TITLE OF INVENTION: ABSENCE OF NONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: Pieh & Richardson, P.C.
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lise A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
                                                                                                                                                                  ADDRE STREET: STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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ZIP: 92037
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Search completed: April 18, 2005, 08:18:35 Job time : 27.2117 secs
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US-09-359-268A-28
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY
TITLE OF INVENTION: THE FIDELITY
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                   SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09359268A Patent No. 6630294
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Best Local Similarity
                                                                                                                                    Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             TYPE: PRT ORGANISM: saccharomyces cerevisiae
                                                                                                                                                                                                                                                 LENGTH: 414
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LENGTH: 971 amino acid
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 LEVQYRMNPYLSEFPSNMFYEGSL 657
                                                                238 LNVQYRMNQKIMEFPSHSMYNGKL 261
                                                                                                   1 LXXQYRMHPXISEFPX---YXGXL 21
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                                                                                                                                                  50.0%;
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                                                                                                                                    1; Mismatches
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Pred. No. 1.
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/1/pubpaa/PCT
2: /cgn2_6/ptodata/1/pubpaa/PCT
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                       / cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep: *
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SUMMARIES
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78 67.5 65.5 65.5 65.5 64.5 64.5 61.5 61.5	Score
775.0 775.0 772.8 772.8 772.8 771.7 771.7 771.7 771.7 771.7 771.7 771.7 771.7 771.7 771.7 771.7	Query Match
21 415 199 734 992 992 472 2231 163 638 638 71 935	Query Match Length DB
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US-10-652-334-6 US-10-652-334-25 US-10-652-334-25 US-10-652-334-25 US-10-424-599-205643 US-10-369-493-2087 US-10-369-493-12790 US-10-652-334-26 US-10-676-701-49859 US-10-479-963-181690 US-10-497-963-181690 US-10-493-963-181690 US-10-493-963-181690 US-10-493-963-181690 US-10-493-963-181690 US-10-493-963-181690 US-10-493-963-181690 US-10-493-963-181690	ID
Sequence 5, App Sequence 25, App Sequence 30872, Sequence 205643 Sequence 2077, Sequence 12790, Sequence 1830, Sequence 18459, Sequence 181690 Sequence 181690 Sequence 1706, Sequence 1706,	Description
6, Appli 25, Appl 25, Appl 20543, A 205643, 2087, Ap 12790, A 26, Appl 1830, Ap 181690, 31794, A 1706, Appli	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
45.5	46	46	46.5		46.5	46.5	47	47.5	47.5	48	52	52	52	52.5	53	53	55	55	57	57	57	57	57.5	57.5	59	59.5	59.5	59.5	59.5	60	60.5
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-10-369-493-	-10-093-463-	-10-094-749	-10-369-493-	US-10-828-924-80	-10-369-493		0-437-963-	-10-369-49		US-10-369-493-4012	US-10-144-194A-22	US-10-144-194A-96	-10-369	96:	-10-369-4	-10-437-963-	59	-10-424-59	-10-437-963-16570	-10-437-96	-10-425-11	-10-424	-10-425-11	-10		US-10-437-963-198010	-369-493-	US-10-437-963-190072	-652-334	-437-963-1	US-10-767-701-57601
Sequence	Sequence	Sequence	Φ			Sequence	Sequence				Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence				Sequence	Seguence	Sequence	æ			Sequence	Sequence	Seguence	Sequence
21645, A	168, App	٠.	1268, Ap	80, Appl	2884, Ap		189923,	22264, A	28, Appl	4012, Ap	22, Appl	96, Appl	2	182704,	2521, Ap	111797,	252174,	202249,	165703,	132395,	45797, A	247410,	43311, A	241211,	118530,	198010,	21526, A	190072,	29, Appl	140079,	57601, A

ALIGNMENTS

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APPLICANT: CZEDIINSKI, KEVIN
APPLICANT: CZEDIINSKI, KEVIN
APPLICANT: DIRMAN, JONACHAN D.
APPLICANT: DIRMAN, JONACHAN D.
TITLE OF INVENTION: A SUBPAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
FILLE OF INVENTION: THEREOF
FILLE OF INVENTION: THEREOF
FILLE OF INVENTION UNMERS: US/10/652,334
CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILLING DATE: 2003-08-28
FRIOR APPLICATION NUMBER: US/09/359,268A
FRIOR APPLICATION NUMBER: 60/093,685
FRIOR APPLICATION NUMBER: 60/093,685
FRIOR APPLICATION NUMBER: 05/093,685
FRIOR APPLICATION NUMBER: 05/093,685
FRIOR FILLING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 21
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                                                                                                                                                                                  ; OTHER INFORMATION: Xaa = any amino acid
US-10-652-334-6
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US-10-652-334-6
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Publication No. US20040115787A1
GENERAL INFORMATION:
                                                                                         Matches
                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                             FEATURE:
                                                                                                            Similarity
                            LXXQYRMHPXISEFPXYXGXL 21
LXXQYRMHPXISBPPXYXGXL 21
                                                                                    86.7%; So ilarity 100.0%; I Conservative 0;
                                                                                                              Score 78; DB 16; 
; Pred. No. 3.3e-07;
                                                                                         Mismatches
                                                                                                                                  Length 21;
                                                                                           Indels
                                                                                         0,
                                                                                         Gaps
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US-10-652-334-25

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                                                                            US-10-424-599-205643
                                                                                              RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: saccharomyces cerevisiae
US-10-652-334-25
              Sequence 205643, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 38822
LENGTH: 199
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Publication No.
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES
TITLE OF INVENTION: THE FIDELITY OF TRANSHATION
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 415
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7426_1.pep
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                         Local
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Local Similarity 62.5%;
les 15; Conservative
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                                                                                                                                                                                                                                                         Similarity
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58.3%;
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0; Mismatches
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Pred. No. 0.00
1; Mismatches
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APPLICANT:

Chen,

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                                                                                                                                       US-10-369-493-12790
                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Schizosaccharomyces pombe US-10-369-493-2087
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION UNMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205643
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2087
LENGTH: 925
                                                                            GENERAL INFORMATION:
                                                                                            Sequence 12790, Application US/10369493 Publication No. US20030233675A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_27723C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(734)

OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                    626
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                                    Gregory J
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Pred. No. 0.
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Pred. No. 0.
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FILE REPERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 12790

LENGTH: 992
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US-10-369-493-12790
                                                                                                                                                                                                                                                                      US-10-369-493-1830
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SEQ ID NO 26
LENGTH: 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/10652334
Publication No. US20040115787A1
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Best Local (
                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBPAMILY OF RN
TITLE OF INVENTION: THE FIDELITY OF
TITLE OF INVENTION: THEREOF
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                          APPLICANT: Cao,
APPLICANT: Hin)
APPLICANT: Slat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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58.3%;
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Pred. No. 0.004;
1; Mismatches
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Pred. No. 0.0027;
1; Mismatches 6;
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OF TRANSLATION
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TERMINATION AND USES
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RESULT 10
US-10-437-963-181690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: LIB3478-020-P1-K1-F11.pep US-10-767-701-49859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-767-701-49859
                           APPLICANT: Li, Ping, TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ.ID NOS: 204966 SEQ.ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1830
LENGTH: 2231
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SEQ ID NO 49859
LENGTH: 163
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                                                                                                                                                                                                                                                                                                               Sequence 181690, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION TOMBER: US/10/767,701
                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
TYPE: PRI
               ENGTH: 638
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                                                                                                                                                                                                                                                        Zhou,
                                                                                                                                                                                                                                                                          Kovalic, David
                                                                                                                                                                                                    Boukharov,
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58.3%;
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58.3%;
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Pred. No. 0.00
0; Mismatches
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ORGANISM: Oryza sativa

FEATURE:

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APPLICANT: Ghosh, Soumitra s.
APPLICANT: Ghosh, Boin D.
APPLICANT: Tahang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
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US-10-408-765A-1706
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Best Local S
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Publication No. US20040101874A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31794
LENGTH: 71
                                                                                          APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                  CURRENT APPLICATION NUMBER: US/10/408,765A
SOFTWARE: FastSEQ for Windows Version 4.0
                    NUMBER OF SEQ ID NOS: 3077
                                                                           FILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO AC003972.1
OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = OTHER INFORMATION: EXPRESSED IN BOUR MARROW.
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_7893C.1.pep
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54.2%;
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IN ADULT LIVER, SIGNAL = 3.8
IN HELA, SIGNAL = 3.3
HIT: Q09820, EVALUE 2.00e-24
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Pred. No. 0.0013;
1; Mismatches 7;
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US-10-767-701-57601
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US-10-474-553-6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1706
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LENGTH: 935
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Best Local Similarity
                    Query Match
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                                                                                                                                                                                      TYPE: PRT ORGANISM: Sorghum bicolor
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                                                                                                                                                                                  FEATURE:
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                                                                                                  FEATURE:
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  67.2%;
58.3%;
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; OTHER INFORMATION: Clone ID: 30969562.pep US-10-767-701-57601
                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE REFERENCE: 38-21(5355)B
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 57601
LENGTH: 219
TURESTH: 219
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Publication No. US20040161765A1

GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING DISEASE
TITLE OF INVENTION: GENES USING NONSENSE-MEDIATED DECAY INHIBITION
FILE REFERENCE: JHY-020.25
CURRENT APPLICATION NUMBER: US/10/474,553
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/283,920
PRIOR APPLICATION NUMBER: 60/283,920
PRIOR FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57601, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(219)
OTHER INFORMATION: unsure at all Xaa locations
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54.2%;
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54.2%;
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Score 60.5; DB 16; Pred. No. 0.0065;
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                       Length 219;
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Sequence 140079, Application US/10437963

Publication No. US20040123343A1

Publication No. US20040123343A1

REMERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

PILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 140079

LENGTH: 1975

TYPE: PRT
ORGANISM: OTYZA SATIVA

PEATURES

OTHER INFORMATION: Clone ID: PAT_MRT4530_41310C.1.pep

US-10-437-963-140079
Search completed: April 18, 2005, 09:04:07 Job time: 75.4964 secs
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                                                                                                                                                                     Query Match 66.7%; Score 60; DB 16; Length 1975; Best Local Similarity 73.3%; Pred. No. 0.085; Matches 11; Conservative 0; Mismatches 4; Indels
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lotosu) whole Blonk (uspto)

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Database
                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                    Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                        DB seq
                                                                                                                                                        length: 0 length: 2000000000
                                                                                                                                                                                                                                       283416 seqs, 96216763 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                  April 18, 2005, 07:32:05 ; Search time 20.2336 Seconds
                                                              PIR_79:*
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pir1:*
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                                                                                                                                                                                                                                                                      Gapext 0.5
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99.861 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	Ħ	Description
۲	67.5	75.0	1121	ָט מ	S30862	DNA dependent ATPa
2	66.5	73.9	1069	N	T43280	nonsense-mediated
ω	65.5		935	N	S62476	hypothetical prote
4	64.5	71.7	2231	N	S53416	SEN1 protein - yea
U	62.5	69.4	1825	N	T52521	related to SEN1 pr
o,	60.5	67.2	1090	N	T00533	probable DNA2-NAM7
7	60.5	67.2	1311	N	T08986	hypothetical prote
80	60	66.7	1687	N	T39072	DNA2-NAM7 helicase
9	59.5	66.1	642	N	D69085	transcription cont
10	59.5	66.1	971	N	S23408	prematurely termin
11	59	65.6	692	N	E90113	hypothetical prote
12	57.5	63.9	660	ผ	F85069	hypothetical prote
13	57	63.3	1075	N	C96682	protein F1E22.16 [
14	55	61.1	2142	N	D86303	F17F16.1 protein -
15	53	58.9	1944	N	T40065	tRNA-splicing endo
16	52	57.8	660	N	T41580	probable dna-bindi
17	50.5	56.1	751	N	C84367	DNA binding protei
18	50	55.6	1076	N	B96682	protein F1B22.14 [
19	47.5	52.8	683	N	S34700	probable purine nu
20	46.5	51.7	650	N	G72429	hypothetical prote
21	46.5	51.7	656	N	E71080	probable DNA-bindi
22	46	51.1	368	μ	FOADMS	minor core protein
23	46	51.1	369	_	FOADM2	minor core protein
24	45.5	50.6	653	N	B75105	probable DNA helic
25	45	ò	246	ผ	P86784	
26	44	48.9	663	N	H64312	
27	43.5	48.3	239	N	T46441	hypothetical prote
28	43.5	48.3	648	N	C69423	DNA helicase homol
29	43	47.8	662	N	E83201	conserved hypothet

RESULT

nonsense-mediated mRNA decay trans-acting factor - Caenorhabditis elegans

ALIGNMENTS

RESULT 1

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S
                                                                                                                                                                                                            A;Cross-referencës: SGD:S0000978; MIPS:YER176w
A;Map position: 5R
C;Keywords: nucleotide binding; P-loop
P;670-677/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9163 and 9132.
A;Reference number: S50679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A; Reference number: $30812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA dependent ATPase/DNA helicase B - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YER176w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S30862
                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: protein
;Residues: 277-283;623-633,'X',635-643 <BI2>
;Comment: This enzyme plays pivotal roles in
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: DNA;Residues: 1-1121 <BIS>;Accession: PC2368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,;Molecule type: DNA
,;Residues: 1-1121 <MUL>
,;Cross-references: UNIPROT:P32644; GB:U18922; EMBL:L11229; NID:g603405; PIDN:AAB64703.1
;Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S30862; S50679; Mulligan, J.T.; Dietrich,
                                                                                                                                                                                                                                                                                                                             Gene: SGD:ECM32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 09-Jul-2004;Accession: S30862; S50679; JC2490; PC2368;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Lomitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                    Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biswas, B.E.; Chen, P.H.; Leszyk, J.; Biswas, S.B. icchem. Biophys. Res. Commun. 206, 850-856, 1895. S.B. icchem. Biophys. Res. Commun. 206, 850-856, 1895. S.B. icchemical and genetic characterization of a replication protein A dependent D: Reference number: JC2490; MUID:95134267; PMID:7832796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S30862;
                                                                                                      Matches
                                                                                                                                                            Query Match
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Residues: 1-1121 <DIB>
Cross-references: EMBL:U18922; NID:g603405; PIDN:AAB64703.1; PID:g603417; MIPS:YER176w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: JC2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S50679
                                                                                                                                  Local Similarity
                                                                                                      15;
                                                1 LXXQYRMHPXISBFP---XYXGXL 21
LDTQYRMHPKISEFPIKKIYNGEL 903
                                                                                                        Conservative
                                                                                                                               75.0%;
62.5%;
                                                                                                      0; Mismatches
                                                                                                                                     Score 67.5;
Pred. No. 0
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                                                                                                                                                         Length 1121;
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C;Species: Sa
C;Date: 05-Ma
C;Accession:
R;Favello, A.
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                 A; Molecule type: DNA
N-Dogidues: 1-2231 <FAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q09820; EMBL:Z54366; NID:g1019812; PIDN:CAA91194.1; PID:g132 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995
A;Residues: 1-2231 <FAV>
A;Cross-references: UNIPROT:Q00416;
                                                               A; Reference number: S53409
A; Accession: S53416
                                                                                                                             R; Pavello, A. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                        8
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A; Residues: 11-935 <BA2>
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A; Accession: T37779
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Mol. Cell. Biol. 19, 5943-5951, 1999
A;Title: SMG-2 is a phosphorylated protein required for mRNA surveillance in Caenorhabdi
A;Reference number: Z22389; MUID:99384262; PMID:10454541
                                                                                                         A; Description: The sequence
                                                                                                                                                                                                                                   N; Alternate names: protein L9576.1; protein YLR430w
                                                                                                                                                                                                                                                         SEN1 protein - yeast (Saccharomyces cerevisiae)
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A;Molecule type: DNA
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A; Accession: S62476
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C;Accession: S62476; T37779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1069 < PAG>
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                                                                                                                                                                       Species: Saccharomyces cerevisiae;Date: 05-May-1995 #text_change 09-Jul-2004;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004;Accession: S53416; A44387; S41985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL: 254366; PIDN: CAA91194.2; Experimental source: strain 972h-; cosmid c16C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
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58.3%;
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se of S. co
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Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65.5; DB 2;
Pred. No. 0.00082;
                                                                                                         cerevisiae
  EMBL:U20939; NID:g664871; PID:g664872; MIPS:YLR430w
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C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision
C;Accession: T52521
                                                                                                                                                                                                                                                             probable DNA2-NAM7 helicase family protein [imported] - Arabidopsis thaliana N,Alternate names: SENI protein homolog T20K24.14 G;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-199 #sequence_revision 01-Feb-199 #text_change 09-Jul-2004 C;Accession: T00533; G84572 C;Accession: T00533; G84572 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R submitted to the EMBL Data Library, July 1997 A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;deMarini, D.J.; Winey, M.; Ursic, D.; Webb, F.; Culbertson, M.R. Mol. Cell. Biol. 12, 2154-2164, 1992
A;Title: SENI, a positive effector of tRNA-splicing endonuclease in A;Reference number: A44387; MUID:92236590; PMID:1569945
A;Accession: A44387
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A;Residues: 'MIS',130,'FCEREVQ',131-2231 <DEM>
A;Cross-references: GB:M74589; NID:g172573; PIDN:AAB63976.1; PID:g172574
A;Cross-references: UNIPROT:O64476; EMBL:AC002392; NID:g3176701; PID:g3176714
A;Experimental source: cultivar Columbia
                                                                                                                                                                                        A; Reference number: Z14167
A; Accession: T00533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related to SEN1 protein [imported] - N; Alternate names: protein B2J23.170
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                                                                                A;Residues:
                                                                                                            A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z26053
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A;Map position: 12R
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                                                                                                                                                        ;Status: translated from GB/EMBL/DDBJ
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                                                                                1-1090 <ROU>
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14; Conserv
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Pred. No. 0.0032;
1; Mismatches 6;
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C;Species: Arabidopsis thaliana (mouse-ear c: C;Date: 11-Jun-1999 #sequence_revision 11-Jun C;Accession: 708986 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1311 <BEV>
A;Residues: UNIPROT:Q9SZW3; EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.130
A;Experimental source: cultivar Columbia; BAC clone F6G3
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A;Cross-references: GB:AE002093; NID:g3176714; PIDN:AAD12029.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA2-NAM7 helicase family protein - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1687 < MUR>
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A;Accession: T39072
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A, Map position: 4
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                                                                                                                                  A; Experimental source: strain
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                                                   Gene: SPDB:SPAC6G9.010c;
                                                                                                                                  ;Cross-references: UNIPROT:Q92355; EMBL:Z81317; PIDN:CAB03612.1; GSPDB:GN00066; SPDB:SF;Experimental source: strain 972h-; cosmid c6G9
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54.2%;
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54.2%;
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Pred. No. 0.00
1; Mismatches
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May 1999
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Query Match

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A;Cross-references: UNIPROT:P30771; EMBL:X62394; NID:g4022; PIDN:CJ R;Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R. M.R. Mol. Cell. Biol. 12, 2165-2177, 1992
A;Title: Gene products that promote mRNA turnover in Saccharomyces A;Reference number: A44388; MUID:92236591; PMID:1569946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Saccharomyces cerevisiae
Cipate: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 09-Jul-2004
Cipate: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 09-Jul-2004
Cipaccession: S23408; A4388; S54455
Rialtamura, N.; Groudinsky, O.; Dujardin, G.; Slonimski, P.P.
J. Mol. Biol. 224, 575-587, 1992
A;Title: NAM7 nuclear gene encodes a novel member of a family of helicases with A;Reference number: S23408; MUID:92235815; PMID:1314899
A;Accession: S23408
                                                                                                                                                                                                                   R;Gentles, S.; Bowman, S. submitted to the EMBL Data Library, May A;Reference number: S54451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9583.05c; protein YMR080c; UPF1 protein
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  A,Cross-references:
                                                                                                                                     A;Residues:
                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M76659; NID:g173141; PIDN:AAA35197.1; PID:g173142
                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-971 <LEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription control factor enhancer-binding protein - Methanobacterium thermoautotroph
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                                                                                 A;Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                              ;Cross-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080c
;Experimental source: strain AB972
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Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                        Accession: A44388
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13; Conserv
                                                                                                                                     1-971 <GEN>
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SGD:S0004685; MIPS:YMR080c
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Pred. No. 0.
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0; Mismatches
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R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an englaved algal nucleus. A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: E90113
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A;Residues: 1-692 <DOU>
A;Cross-references: UNIPROT:Q9AVZ7; GB:AJ010592; NID:g12580756; PIDN:CAC27074.1;
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C;Keywords: GTP binding; mitochondrion; nucleotide binding; nucleus; P-loop
F;430-437/Region: nucleotide-binding motif A (P-loop)
F;545-548/Region: GTP-binding NKXD motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AT4g05540 [imported] - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Date: 18-69b-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: P85069
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C; Keywords: nucleomorph
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                                                                                                                                                                                              A;Map
                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9S9W3; GB:NC_001268; NID:g7267314; PIDN:CAB81096.1;
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A; Residues: 1-660 <STO>
                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                  A; Accession: F85069
                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and analysis of chromosome 4 of the plant A; Reference number: A85001; MUID: 20083488; PMID: 10617198
                                                                                                                                                                                                                                                                                                                                                                                      Nature 402, 769-777,
                                                                                                                                                                                                                                                                                                                                                                                                            R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold
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                                                                          LXXQYRMHPXISEFP---XYXGXL 21
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54.2%;
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                                                                                                                                     Score 57.5; DB Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 2;
Pred. No. 0.0092;
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tRNA-splicing endonuclease positive effector - C;Species: Schizosaccharomyces pombe
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Kh C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros Rizzo, M.; Rooney, T.; Rowley, T.; Kokar, J.R.; Shinn, P.; Southw A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southw A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southw A;Title: Sequence and analysis of chromosome 1 of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Theologis, A.; Baker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, T.; R
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                                                                                                                                                                                                                                                                                                                                                      A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: D86303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A86141;
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                                                                                                                                                            Local
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Arabidopsis thaliana (mouse-ear cress)
                                                                                                                          l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                               1-2142 <STO>
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                                                               LXXQYRMHPXISEFP 15
LTQQYRMHPBICRFP
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                                                                                                                                                            61.1%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUID:21016719; PMID:11130712
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                                                                                                                                                            Score 55; I
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                        GB:AE005172; NID:g9954728; PIDN:AAG09081.1; GSPDB:GN
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                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Federspiel, N.A.; Kaul, S.; White, O.; Alo
y, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                         Length 2142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.; Khan, S.; ; Luros, J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Southwick, A.M.; Sun,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khaykin, B. Maiti, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khaykin, E
Maiti, R.;
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tallon,
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fission yeast

(Schizosaccharomyces

pombe)

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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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O7rq16 plasmodium
O7rq16 plasmodium
O6c803 yarrowia li
D32644 saccharomyc
O9fjr0 arabidopsis
O863k7 arabidopsis
O76512 caenorhabdi
O6fkf3 candida gla
O09820 schizosacch
O8tfw3 aspergillus
O6myi2 aspergillus
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004 004 1128 1128 7XX	ິ່ນທີ	SEQUENCE FROM MEDLINE=22255 Gardner M.J., Carlton J.M., Eisen J.A., R. Chan M.S., Net Chan M.S., Net Pertea M., Al. Martin D.M., Martin D.M., Martin D.M., McFadden G.I., Venter J.C., Fraser C.M., Fraser C.M., Fraser G.M., Nature 419:49 EMBL, AB01482; SEQUENCE 15	D # # # 7 000	61.5 60.5 60.5 60.5 60.5 60.5 60.5 60.5 60
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1297 AA.) quence update) notation updat ated. Haemosporida;	re 70; DB 2; Length 15 d. No. 0.0011; Mismatches 4; Indels	OOI=10.1038/nature co.) Berriman M. Bowman S., Paulse S.L., Craig A., K in B., Peterson J. ift D., Mather M. Iz M.J., Roos D.S. nanian G.M., Munga S.L., Newbold C., la parasite Plasmo	1554 AA. quence update) notation updat putative. Haemosporida;	1 HUMAN U62 WT0 GY0 U83 U83 HU9 HU7 HU7 U90 ZU0 ZU0 ZU0 SCHPO 671 ALIGNMENTS
e) Plasmodium.	1554; els	reol097; W., Hyman R sen I.T., Ja Kyes S., Angivol: K, Vaidya S., Ralph S yall C., Davis R.W modium	e) Plasmodium.	092900 07qu62 06bwt0 09fgy0 09ff83 09fhu6 09fhu7 09fhu6 09fhu6 09fav3 09szw3 074zu0 074zu0 07355
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Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
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                Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382130; CAG81409.1;
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR011545; DEAD/DEAH_N.
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Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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Yarrowia lipolytica chromosome D of strain CLIB99 o
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                                                                                                                                                                                                                           STRAIN=CLIB99;
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L; AABL01000336; EAA20580.1;
L; 7097 AA; 149791 MW;
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                                                                                                                                                                                                                                                                                                                   430:35-44 (2004).
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70.6%;
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Pred. No. 0.002;
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                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Aviles B., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
Hypothetical 127.0 kDa protein in RAD24-BMH1 in
OrderedLocusNames=YER176W; ORFNames=SYGP-ORF61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00487; DEXDC; 1.
ATP-binding.
SEQUENCE 964 AA; 10776
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."; Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288c / AB972;
MEDLINE=97313264; PubMed=9169868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                          GO:0005844; C:polysome; IDA.
GO:0003678; F:DNA helicase activity; IDA.
GO:0006449; P:regulation of translational
erPro; IPR001410; DEAD.
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                                                                                                                                                                                                                                                              al protein. (Potential)
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01-JUN-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                               Q8S3K7
Johzuka Y., mulligan M.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP44122; AAL92018:1; -.
GO; GO:0015668; F:type III site-specific deoxyribonuclease
GO; GO:0009307; F:DNA restriction; IEA.
                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Regulator of nonsense transcripts 1 homolog.
OrderedLocusNames=At5g47010; ORFNames=MQD22.15;
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InterPro; IPR006935; ResIII.
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                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
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2 (TrEMBLrel. 21,
3 (TrEMBLrel. 24,
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148 178 (C2H2-type (atypical) (Potential).
202 232 C4-type (Potential).
507 514 ATP (Potential).
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Pred. No. 0.0024;
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177B3F6C524D2E6A CRC64
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076512; Q9BL16;

16-OCT-2001 (Rel
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                                                                  ZN_FING
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Wormbep; Y48GBAL.6; CE28367. 
InterPro; IPR003593; AAA, AIPase. 
InterPro; IPR006935; ResIII. 
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                      EMBL; AF074017; AAC26789.1; -.
EMBL; AC025721; AAK29903.2; -.
PIR; T43280; T43280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page M.F., Carr B., Anders K.R., Grimson A., Anderson P.; "SMG-2 is a phosphorylated protein required for mRNA surveillance Caenorhabditis elegans and related to Upfip of yeast."; Mol. Cell. Biol. 19:5943-5951(1999).
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NON_TER 1 1
SEQUENCE 1243 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform investigating biology,"; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND MUTAGENESIS OF MEDLINE=99384262; PubMed=10454541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Regulator of nonsense transcripts 1 (Nonsense
                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation.
-!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.

    -I- FUNCTION: Eliminates the production of nonsense-containing RNAs
    -I- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
    -I- PTM: Phosphorylated. Smg-1, smg-3 and smg-4 are required for

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Up-frameshift suppressor 1 homolog).
Name=smg-2; ORFNames=Y48G8AL.6;
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                                                                                                                 Hydrolase; Phosphorylation;
C2H2-type (atypical)
C4-type (Potential).
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                                         ATP (Potential Gln/Ser-rich. Poly-Thr.
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MBL outstation -
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Joyethof E., Wirth B.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Weincher G., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome L complete sequence.
ORFNames=CAGL0L12034g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6FKF3;
               Schizosaccharomyces pombe (Fi
Eukaryota; Fungi; Ascomycota;
                                            Regulator of nonsense ORFNames=SPAC16C9.06c;
                                                                      16-OCT-2001
05-JUL-2004
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Eukaryota; Fungi; Ascomycota;
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 Schizosaccharomycetales;
                                                                                                     01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                    Wincker P.,
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                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                                                                                                                                                                                                     "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQVQYRMHPVLSEFPSNVFYDGSL 695
                                                                                                                                                                                                          LNTOYRMHPTISEFP 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1069
                                                                      (Rel. 32,
(Rel. 40,
(Rel. 44,
                                                                                                                                                                                                                                                                                                                             1125 AA;
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                           CAG62265.1; -.
AA; 127137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472
                             pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                               73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120019
                                                       Last annotation update) transcripts 1 homolog.
                                                                      Last sequence update)
Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HE -> QQ
S -> P (i
MW; 5B4C9
                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:
                                                                                                                                                                                                                                                                                Score 66; DB 2;
Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66.5; DB 1;
Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G->E: In R895; loss of activity and increased phosphorylation.
HE -> QQ (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increased phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
             Schizosaccharomycetes;
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5B4C91FB49B5C24B CRC64
                                                                                                                                                                                                                                                                                                                             63C0428123F3CC8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (in Ref.
                                                                                                                                  925 AA
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                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                             Length 1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1069;
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'
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RESULT 10
Q8TFW3
ID Q8TFW
AC Q8TFW
DT 01-JU

Q8TFW3; Q8TFW3; 01-JUN-2002

(TrEMBLrel.

21,

Created)

PRELIMINARY;

PRT;

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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones H., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S.,
RA Goliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Golaves S., Stevens K.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Whitehead S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Eger P., Ziddieu S., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu S., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
The genome sequence of Schizosaccharomyces pombe.";
RT The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                   Matches
                                                                                                                                                                      Best Local
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: Eliminates the production of nonsense-containing
-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-1- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00487; DEXDC; 1.
ATP-binding; Helicase; Hydrolase; Hypothetical protein;
Nonsense-mediated mRNA decay; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z54366; CAA91
PIR; S62476; S62476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GeneDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR003593;
                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00382; AAA;
SM00487; DEXD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPombe; SPAC16C9.06c;
                                                                                                                                                                      Similarity
                                                                 LXXQYRMHPXISEFPX---YXGXL
   LVVQYRMHPCLSEFPSNTFYEGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR006935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001410;
                                                                                                                                                                                                                                                                      414
925 AA;
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA91194.2; -.
                                                                                                                                                                                                                                                                      104528 MW;
                                                                                                                                                               72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ResIII.
                                                                                                                                                                                                                                                                   C2H2-type (atypical)
C4-type (Potential)
ATP (By similarity)
MW; 4A5D63C82826E864 C
                                                                                                                               1; Mismatches
                                                                                                                                                                      Score 65.5; DB 1
Pred. No. 0.0041;
   649
                                                                 21
                                                                                                                                                                                                                                                                                                                                                                (atypical)
                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
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SORRETT A
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Best Local
                                                     Matches
                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                               PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;
Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M. Posker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S., O'Neil S., Pertea M., Price C., Rabbinowittsch E., Rajandream M-A., Salzberg S., Saunders D., Seegar K., Sharp S., Warren T., Denning D.W., Barrell B., Hall N.;
"Insight into the genome of Aspergillus fumigatus: analysis of a 922 kb region encompassing the nitrate assimilation gene cluster."; Rungal Genet. Biol. 41:443-453 (2004).
EMBL; BX649506; CAF32021.; -
InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR01545; DEAD/DEAH_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus (Sartorya fumigata).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knowles D.G., Warren T., Hall N., Quail M., Woodward J.R., Denning D.W., Anderson M.J., Barrell B.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AL713629; CAD28448.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible regulator of nonsense transcripts.

Name=AEA5C11.22c;

Aspergillus fumigatus (Sartorya fumigata).

Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
PubMed=14998527; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulator of nonsense transcripts, putative ORFNames=AfASc11.22c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003593; AAA ATPase.
InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR006935; ResIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6MYI2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04851; ResIII; 1.
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                                                                                                                                                                 SEQUENCE
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO:0000166; F:nuclectide binding; IEA.
GO:001566; F:type III site-specific deoxyribonuclease ac. ..;
GO:0009307; P:DNA restriction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634
                                                                                                                                                                                                           PF04851; ResIII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                     14;
                                                                                                                                                                                             SM00487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                 Similarity
  LXXQYRMHPXISEFPX---YXGXL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNVQYRMHPCLSEPPSNMFYEGSL 657
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                                                                                                                                                                 1079 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1060 AA;
                                                     Conservative
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                                                                                                                                                                                       DEXDc; 1.
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                                                                            72.8%;
58.3%;
                                                                                                                                                                 118655 MW; A8907E6FA8500E63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65.5; DB 2;
Pred. No. 0.0047;
1; Mismatches 6;
                                                  1; Mismatches
                                                                            Score 65.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744DFC58A26EE77B CRC64;
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                                                                               0.0048;
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                                                                                                     Length 1079;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus.
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T
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RESULT 12
RNT1_NEUCH
    RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butter J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butter J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butter J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Koy A., Foley K., Naylor J.,
RA Macuser Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M.,
RA Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
RA Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Birern B.,
RT The genome sequence of the filamentous fungus Neurospora crassa.";
RI Nature 422:859-88(2003).
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Q9HEH1; Q7RVU9;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
05-JUL-2004 (Rel. 4
                         use by non-profit institutions as lone modified and this statement is not remove entitles requires a license agreement (SG or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Regulator of nonsense transcripts 1 homolog.
ORFNames=2E4.130, NCU04242.1;
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Nonsense-mediated mRNA
ZN_FING 111 139
ZN_FING 163 193
ZN_BIND 477 484
                                                                                                                                                             EMBL; AL451022; CAC18314.1; -.
EMBL; AABX01000272; EAA31997.1; -.
InterPro; IPR003593; AAA ATPA86.
InterPro; IPR001410; DBAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=74-OR23-1A / FGSC 987;
PubMed=12712197; DOI=10.1038/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "What's in the genome of a filamentous
Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).

    -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
    -!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Eliminates the production of nonsense-containing RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653
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                                                                                                                                                                                                                                                                                                      rmatics Institute. There are no restrictions institutions as long as its content is in attement is not removed. Usage by and for con
C2H2-type (atypical) (Potential).
C4-type (Potential).
ATP (Potential).
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Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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25-OCT-2004
25-OCT-2004
Q7LIE9
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Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouchier C., Caudron B., Scarpelli C., Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genotevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                         ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CR382137; CAG88524.1; -
GO; GO:000166; F:nucleotide binding;
InterPro; IPR003593; AAA ATPase.
InterPro; IPR001547; GlyGo_hydro_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                     12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        SM00382; AAA;
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                                                                                                                                                                                                                                                                                                                                                             PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
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(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
hansenii chromosome B of strain CBS767
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  PRELIMINARY;
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58.3%;
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73
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80.0%;
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                                                                                                                                                                                                                     Score 65; DB
Pred. No. 0.00
0; Mismatches
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Pred. No. 0.0049;
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W; 8B0E4F0407ACE142 CRC64;
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     PRT;
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RESULT 15
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnston M., Hiller L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Louis B.J., Messenguy F., Mewes H.W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleoide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                  Q6FK55;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                       Candida glabrata CBS138.

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; mitosporic Saccharomycetales;
                                                                                                                                                                                                       Candida glabrata strain ORFNames=CAGLOM00990g;
                                                                                                                                                                                                                                                                               05-JUL-2004
05-JUL-2004
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                          STRAIN=CBS138;
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                                                                                             NCBI_TaxID=284593;
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RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvegilse C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Miller H.,
RA Nicaud J.M., Nikolaki M., Oztes S., Ozter-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Semenene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Wincher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincher P., Souciet J.L.,
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RA Wincher 1979 AA; 224955 MM; A38F91B1F8E7CDFE CRC64;
Best Local Similarity 58.3%; Pred. No. 0.014;
Matches 14; Conservative 1; Mismatches 6; Indels 3; Gaps 1;
Db 1610 LDVQYRMHPAISKFPSAEFYDGRL 1633

Search completed: April 18, 2005, 08:15:46

Job time: 88.6788 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	80	ID	Description
1	47	87.0	171	ωį	AAB33009	Aab33009 Pinus rad
N	46	5	14	7	ABW01183	Saccha
ω	46	•	14	æ	ADP44109	_
4	46	85.2	15	w	AAY77810	Motif
տ	46		648	8	ADS42927	Bacter
0	46		1944	8	ADN19868	Adn19868 Bacterial
7	45		1274	4	ABB65781	Abb65781 Drosophil
89	44	81.5	125	7	ADB63936	
ø	44		414	w	AAY77816	Yeast
10	44	81.5	414	7	ABW01204	Saccha
11	44	81.5	414	8	ADP44130	_
12	44	81.5	517	σ	ABB99784	Amino
13	44		550	σ	ABB99781	Abb99781 Amino aci
14	44	81.5	683	8	ADS43834	Ads43834 Bacterial
15	44		804	7	ADB65007	-
16	44	81.5	1002	s	ABB79913	Abb79913 Arabidops
17	44		1187		AAU07865	Aau07865 Polypepti
18	44		1208	σ	ABB99782	Abb99782 Amino aci
19	44		1211	4	AAU07886	Aau07886 Polypepti
20	44	81.5	1315	σ	ABJ19762	
21	44		1349	6	ABB99783	Abb99783 Amino aci
22	44		1942	7	ADE59894	Ade59894 Human Pro
23	43		338	σ	ABJ19763	Abj19763 Human MP2
24	43	79.6	642	æ	ADS43096	Ad843096 Bacterial
25	43	79.6	650	8	ADN20231	Adn20231 Bacterial

The present invention relates to novel plant transcription factors from Bucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a plant having secala, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide.

WPI; 2000-579369/54.

Wood M,

Mcgrath A,

Shenk MA, Glenn M;

Claim 8; Page 390; 747pp; English.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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Aaw89879	Abp07670	Abg41302	Abg53184	Aam58962	Aam71489	Abb23527	Aam31789	Abb38350	Aam19141	Abb71759	Abg29081	Abg17826	Abg18338	Adp44113	Abw01187	Abo62362	Adp44127	Abw01201	ABY / /BI3
Antigen 2	Human ORF	Human per	Human liv	Human bra	Human	Protein #				Drosophil		Novel hun	Novel hum	Yeast	Saccharon	Klebsieli		Saccha	Yeast Mtt

ALIGNMENTS

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Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZTI; G-box binding factor; basic helix-loop-helix zipper; homeocic; homeocdomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                                                                                      11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                09-MAR-2000; 2000WO-US006112.
                                                                                                                                                                                                                                                                                                                                    Pinus radiata transcription factor protein sequence #136.
                                                                                                                                                                                                                                                                                                                                                                      AAB33009;
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                                                                                                                                                                                                                                                                  Pinus radiata.
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99US-0149485P.
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RESULT 2
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Best Local (
                     The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide
                                                                                                                                                                                                                                                                                                    Identifying therapy, by
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                                                                                                                                                                                                          Disclosure; Col
                                                                                                                                                                                                                                                      binding to Mttl.
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contacting modulator of translation termination (Mttl)
es cerevisiae with a test agent, and detecting specific
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Pred. No. 0.
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Best Local S
modulates the efficiency of translation termination composition the RNA helicase MTT1 with a composition or agent under conditions permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1, and determining if the test composition or agent inhibits the MTT1. The composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, permit monitoring of a termination event, promote degradation
                                                                                                                                                                                                                                                                                                                                                                            translation t
composition o
inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14
                                                                                                                                                                                                                                                                                                                   Claim 39; SEQ ID NO 7; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-449400/42.
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22-JUL-1999;
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                                                                                                                                                                                                                                                            The invention relates to a method of identifying a test composition that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004115787-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; translation termination; RNA helicase; MTT1;
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) CZAPLINSKI K.
) DINMAN J D.
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Pred. No.
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The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in
                                                                                                                                                                                                  New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia;
                                                                                                                                                                    Claim 39; Page 80; 89pp; English.
                                                                                                                                                                                                                                                                                 WPI; 2000-171458/15
                                                                                                                                                                                                                                                                                                                   Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1998;
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/note= "reisdues indicated Xaa
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RESULT 5
ADS42927
ID ADS4
XX ADS4
XX ADS4
XX ADS4
XX ACC
XW COLC
XW COLC
XW COLC
XW DACH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved i peptidyl transferase activity during translation, inhibiting the interaction, between MTT1 and eRF3 or involved in enhancing translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                             (CAOY/)
(HINK/)
(SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
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                                                            WPI; 2004-061375/06
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                                                                                                                                                                                                             HINKLE G
SLATER S
CHEN X.
                                                                                                                     Hinkle GJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorus; photosynthesis; lignin;
polypeptide.
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Pred. No.
                                                                                                                           Chen
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                                                                                                                           Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
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New recombinant DNA construct comprising a promoter positioned to provide

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RRESULT 6
ADN19868
ID ADN19868
ID ADN19868
AC ADN1
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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    (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nitrogen;
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                                                                                                                                      (CAOY/)
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    CAO Y.
HINKLE G
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CHEN X.
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polypeptide.
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71.4%;
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Pred. No. 0.54;
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IGVVTPYRSQVQQL 1684

Query Match Best Local & Matches

Local Similarity mes 9; Conserv

Conservative

85.2%;

Score 46; DB Pred. No. 1.9;

8 4

Length 1944;

Indels

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Gaps

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Mismatches

Sequence

1944 AA;

RESULT 7
ABB573
ABB574
ABB574
AC ABB6
XX ABB6
XX ABB6
XX Dros

pharmaceutical

Drosophila melanogaster.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE) PE CORP NY

23-MAR-2001; 2001WO-US009231

27-SEP-2001 WO200171042-A2 Drosophila melanogaster polypeptide SEQ ID NO 24135

Drosophila; developmental biology; cell signalling; insecticide;

ABB65781;

26-MAR-2002

(first entry

ABB65781 standard; protein; 1274 AA

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CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC content, improved plant growth and development under at least one stress CC condition, improved plant growth and development under at least one stress CC condition, improved lignin production of photosynthesis or by CC production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not CC form part of the printed specification but was obtained in electronic CC format from USPFO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maire or soybean. The method of producing a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polyneptide from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GOLD/) GOLDMAN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2521; 122pp; English.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosphila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                           Seki N,
                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1308459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein encoded by clone BRACE20200770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB63936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB63936 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                       Yamamoto
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                                                                                                             2003-450961/43.
DB; ADB61966.
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RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                           J, Isono
Yoshikawa
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                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 125
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64.3%;
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                                                                                                                                                                                        Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWD,
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Pred. No.
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                                                                                                                                                                                                                                                Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                                          Tamechika
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a polymucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide CC of the polymucleotide, immunologically assaying the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC with the antibody of the encoded protein, and observing the binding CC expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide, or as a probe CC is useful as a primer for synthesising the polymucleotide, or as a probe CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets of genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets of genes therapy. The genes are involved in tissue and/or cell cranscription-related proteins, disease-related proteins, and genes are involved in transduction-related proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                         WPI; 2000-171458/15
                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY77816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77816 standard; peptide; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast Dip1
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                                                                                                             Peltz S,
                                                                                                                                                                                    22-JUL-1998;
                                                                                                                                                                                                                       22-JUL-1999;
                                                                                                                                                                                                                                                                                                WO200005586-A2
                                                                                                                                                                                                                                                                                                                                                                         helicase; Dipl.
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                                                                                                                                                  (UYNE-) UNIV NEW JERSEY
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                                                                                                             Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein fragment.
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                                                                                                                                                                                      98US-00120435
                                                                                                                                                                                                                           99WO-US016802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
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                                                                                                             Dinman
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Pred. No. 0.22
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               eRF3;
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New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.

Example 1;

Fig 1; 89pp; English.

invention

provides a new multiprotein complex which can modulate

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 termination. Vectors comprising polynuclectides encoding the complex (or antisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant transcripts in a cell. Agents binding to the complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation termination of mRNA at a nonsense codon and/or promote degradation of aberrant transcripts in cells. The method can be used to identify agents/compositions modulating binding to MTTI, useful to identify genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved in peptidyl transferase activity during translation, inhibiting the proportion of defection the complex before a peptidyl transferase activity during translation, inhibiting translation of the proportion of the complex before the complex before transferase activity during translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It
WPI; 2003-810549/76.
                                                                                                                                                                                                     07-OCT-2003.
                                                                                                                                                                                                                                                                                    Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABW01204 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 414
                                       Peltz S,
                                                                                                                                                               22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                               Modulator of translation termination; MTT1; helicase B; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAY77813-817 represent protein fragments from yeast superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
9; Conserva
                                                                               UNIV NEW JERSEY MEDICINE & DENTISTRY
                                       Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGVISPYNAQVSHL 355
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae DIP1 protein.
                                                                                                                       98US-0093685P
                                                                                                                                                               99US-00359268.
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                                                                                                                                                                                                                                                                                                                          mutation; yeast
                                       Dinman JD
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Pred. No. 0.88;
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Best Local
                                                             Identifying a test composition or agent that translation termination comprises contacting composition or agent, and determining if the inhibits the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beat thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Nederly Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTI) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae DIP1 protein
                                                                                                                                                                                                                                                                   22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast helicase Dipl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                Disclosure;
                                                                                                                                             WPI; 2004-449400/42
                                                                                                                                                                          Peltz S,
                                                                                                                                                                                                      (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
(DINM/) DINMAN J D.
                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                US2004115787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 55-58; Opp; English.
                                                                                                                                                                                                                                                                                                                  28-AUG-2003; 2003US-00652334.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurofibromatosis; Retinoblastoma; ATM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                        Czaplinski K,
                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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99US-00359268
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                              28; 41pp; English
                                                                                                                                                                            Dinman JD
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Pred. No. 0.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Costmann Disease;
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                                                                                                              modulates the efficiency of
                                                                               the MTT1 with test composit:
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The invention relates to a method of identifying a test composition that

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ID ABBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAMP; cardiac helicase activated by MEF2 protein; cardiomyocyte; cardiac function; heart; myocardial infarction; heart failure; cardiac hypertrophy; exercise tolerance; cardiac hypertrophy.
                                                                                                                                                                                   New CHAMP (cardiac helicase activated by MEF2 protein) polypeptide and polynucleotide, useful for enhancing cardiac function for treating, inhibiting progression of or preventing myocardial infarction or heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2001; 2001US-0269764P.
24-JAN-2002; 2002US-0351713P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olson
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Pred.
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The present sequence represents a polypeptide, designated CHAMP (cardiac

The present sequence represents a polypeptide, designated CHAMP (cardiac helicase activated by MBF2 protein). The CHAMP protein contains seven conserved motifs bearing a striking resemblance to RNA helicases involved in RNA processing, and to enhancer binding factors involved in tissue transcription. CHAMP is expressed in cardiomyocytes from the linear tube stage to adulthood. The CHAMP polymucleotide is useful for enhancing cardiac function in a mammal. The CHAMP polypeptide and polymucleotide are particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particularly useful for increasing CHAMP activity in the heart or the particular than the particular t

of a subject,

order to treat,

inhibit progression of or

Claim 2; Page 117-118; 133pp; English

Claim 2; Page 132-133; 133pp; English

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RESULT 13
ABB99781
ID ABB99781
AC ABB99
XX AMINC
AC ABB99
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XX CHAME
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                                                                                                                                                                                                                                                                                                                                                                                                   New CHAMP (cardiac helicase activated by MEF2 protein) polypeptide and polynucleotide, useful for enhancing cardiac function for treating, inhibiting progression of or preventing myocardial infarction or heart
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24-JAN-2002; 2002US-0351713P.
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Pred. No. 1.1;
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                      The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant thaving an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant with the recombinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination, seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevent myocardial infarction, heart failure or cardiac hypertrophy. is also useful for inproving quality of life, decreasing morbidity, or decreasing mortality in a subject with heart failure or cardiac
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tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
Sequence 683 AA;
                                                                                                                        format from USPTO at seqdata.uspto.gov/sequence.html.
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Human protein
                                                                               04-DEC-2003
                                                                                      ADB65007 standard; protein; 804
                                                                               (first entry)
                                                                           encoded by clone PUAEN20002470
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Human; pharmaceuricell regeneration; Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related proternscription-related protein; osteoporosis; neurological disease; protein;

EP1308459-A2 Homo sapiens.

05-NOV-2001; 25-JAN-2002; 28-MAR-2002; 07-MAY-2003 2001JP-00379298. 2002US-00350978. 2002EP-00007401

Yamamoto (REAS-) Isogai T, HELIX RES INST.
RES ASSOC BIOTECHNOLOGY. J, Isono Yoshikawa Sugiyama T, Ήĸ Otsuki T, Hio Y, Ots Otsuka M, T, Wakamatsu A, Otsuka K, Nagai M, Nagahari K, I Masuho ζ, Sato H, Irie ho Y; ₽, Ishii S; Tamechika

marker or medicines as targets of gene t New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or therapy.

N-PSDB;

2003-450961/43.

ADB63037.

Claim 1; Page; 222pp; English.

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding

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cc between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotide and encoded composed the polynucleotide and encoded composed in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell composed therapy. The genes are involved in tissue and/or cell cregeneration. Membrane proteins, signal transduction-related proteins, composed to transcription-related proteins, disease-related proteins and genes concoding them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed composed patent of the invention supplied by the
                                                                                                                                                                                                                                                                                                                                           Sequence 804 AA;
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1 IGVITPYXXQV 11
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702 IGVITPYRKQV 712
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Issued Patents Ah:*
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               US-09-359-268A-7
US-09-359-268A-28
US-09-359-092-488
US-09-248-796A-15170
US-09-359-268A-25
US-09-359-268A-21
US-09-359-268A-21
US-09-359-268A-11
US-09-359-268A-11
US-09-270-767-41521
US-09-270-767-41521
US-09-270-984A-22
US-09-270-984A-22
US-09-177-431-8
US-08-724-354D-4
US-08-724-354D-4
US-08-724-354D-2
US-09-270-984A-2
US-09-270-984A-2
US-09-270-984A-2
US-09-270-984A-2
US-09-270-984A-2
US-09-270-984A-19107
US-09-288-796A-19107
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10148, Appl
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56745, A
41521, A
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7, Appli
28, Appl
483, App
15170, A
25, Appl
8879, Ap
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19347, A
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RESULT 1 US-09-640-211A-1058 ; Sequence 1058, Appli ; Patent No. 6833446 ; Patent IMPORMATION: ; APPLICANT: Wood, Ma APPLICANT: Shenk, ; APPLICANT: Grath		45	44	&	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	
211A- 1058 0. 68 0. 68 NT: W		32	32	32	32	3 2	32	32	32	32	33	ü	ω ω	33	33	33	33	34	34	
1A-1058 058, Application US 0833446 FORMATION: Wood, Marion Shenk, Michael A		59.3	ø	9	59.3	59.3	59.3	59.3	59.3	59.3	61.1		•	•	61.1	61.1	61.1	63.0	63.0	
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SULT 1 -09-640-211A-1058 Sequence 1058, Application US/09640211A Sequence 1058, Application US/09640211A GENERAL INFORMATION: APPLICANT: Wood, Marion APPLICANT: Wood, Marion APPLICANT: McGraft, Annette	ALIGNMENTS	US-08-747-863-2	US-08-157-005-2	US-09-387-695-2	US-09-583-110-5097	US-09-489-039A-11458	US-09-134-000C-5430	US-09-270-767-44821	US-09-489-039A-12183	US-09-107-433-3408	US-09-252-991A-24623	US-09-489-039A-13843	US-09-438-185A-402	US-09-198-452A-419	US-09-248-796A-16115	US-08-311-731A-265	US-09-359-268A-20	US-09-581-345-5	US-09-902-540-13130	
		Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence		Sequence	Sequence	Sequence	Sequence	
·				2, Appli	5097, Ap	_	5430, Ap	44821, A	•	3408, Ap	24623, A		402, App		16115, A	265, App	20, Appl	5, Appli	13130, A	

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Sequence 7, Application US/09359268A

Patent No. 6630294

GENERAL INFORMATION:
APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-65N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT PILING DATE: 1999-07-22
PRIOR APPLICATION UNUMBER: 60/093,685
PRIOR APPLICATION UNUMBER: 60/093,685
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-1058
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APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ.ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1058
LENGTH: 171
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Pred. No. 0.
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US-09-538-092-483
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US-09-359-268A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-359-268A-28
                                                                           SEQ ID NO 483
LENGTH: 683
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Patent No. 6753314
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APPLICANT: Giot, Loic
APPLICANT: Mansfield,
                                                                                                             PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version 0.9
                                                                                                                                                                            TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542 CURRENT APPLICATION NUMBER: US/09/538,092 CURRENT FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: 60/127,352 PRIOR FILING DATE: 1999-04-01
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 32
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CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
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PEATURE: misc_feature LOCATION: (0)...(0)
                                             TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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THE FIDELITY OF TRANSLATION '
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Pred. No.
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Pred. No. 0.48;
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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PELICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15170
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15170
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APPLICANT: Czaplinski Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: THE FIDELI
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15170, Application US/09248796A Patent No. 6747137
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                                                                                                                         TYPE: PRT ORGANISM: saccharomyces cerevisiae
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1 IGVITPYXXQ 10
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Pred. No. 0.83;
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US-09-489-039A-8879
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                                                           US-09-270-767-56745
                                                                                RESULT
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SEQ ID NO 8879
LENGTH: 1176
                            Sequence 56745, Application US/09270767 Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 11
LENGTH: 10
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Best Local Similarity
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APPLICANT: Gary Br
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 601-1-85N
CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
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TITLE OF INVENTION: A SUBFAMIL
TITLE OF INVENTION: THE FIDELI
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-22
 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                     ORGANISM: saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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              INFORMATION:
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Homburger et al
                                                                                                                                                                   IGVITPYXXQ 10
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                                                                                                                                  IGVITPYXAQ 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czaplinski, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peltz, Stuart
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90.0%;
                                                                                                                                                                                                                                                                                     any amino acid
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Pred. No. 0.035;
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US-09-359-268A-29
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APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY
TITLE OF INVENTION: THE FIDELIT
TITLE OF INVENTION: THERROP
FILE REFERENCE: 601-1-85N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094 CURRENT FILING DATE: 1999-03-17 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 41521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41521, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
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Matches
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CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56745
LENGTH: 238
                                                                                                                                                                                                                                                                                            Patent No. 6030-100:
                                                               SOFTWARE:
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09359268A Patent No. 6630294
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Best Local :
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                                                                                                                  CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22 PRIOR APPLICATION NUMBER: 60/093,685 PRIOR FILING DATE: 1998-07-22
                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Homburger et al.
   LENGTH: 380
TYPE: PRT
ORGANISM: saccharomyces cerevisiae
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TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
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7; Conserva
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7; Conserv
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Pred. No. 2.
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Pred. No.
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US-08-724-354D-22
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US-09-248-796A-19347
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US-09-248-796A-19347
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                  equence 22, Application US/08724354D atent No. 5994119
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                                                                                                                                                                                                                    ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                    SOFTWARE: PastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                      FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                      FILING DATE: 01-OCT-
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            STREET: Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.1%;
Local Similarity 70.0%;
nes 7; Conservation
              NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                 COMPUTER: IBM CONCERNING SYSTEM:
                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                       APPLICATION NUMBER: 60/016,482
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                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                 IBM Compatible
SYSTEM: Windows95
                                                                                                                                                                                                                 Diskette
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80.0%;
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              RESULT 15
US-09-177-431-8
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Sequence 8, Application US/09177431
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haile, Liea A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                      Local
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                                                                            726
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                                                                                                         1 IGVITPYXXQ 10
                                                                                                                                  n 74.1%;
Similarity 80.0%;
8; Conservative
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                                                                            IGVITPYEGQ 735
                                                                                                                                                                                                                                                             971 amino acids
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                                                                                                                                                                                                                                                                                                             619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietz, Harry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                             619-678-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
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80.0%;
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Sequence 22, Application US/09270984A
                                                                                                                                                                                                                                                                                                                              COMPUTER: 15M COMPUTER: Windows95
OPERATING SYSTEM: Windows95
OPERWARE: FASTSEQ for Windows Version 2.0
OPERWARE: PASTSEQ FOR WINDOWS VERSION 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Fish & Richardson, P.C.
4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                  08/724,354
                                                                                                                                                                                                                                                                                                                           US/09/270,984A
                                                                                                                                                                                                         07265/090001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB Pred. No. 8.1;
             Pred. No. 8.1
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 971;
                           Length 971;
 Indels
0
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Gaps
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 0
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iENGTH: 971 amino acids
iTYPE: amino acid
iPOPOLOGY: linear
iMOLECULE TYPE: protein
iPRAGMENT TYPE: internal
US-09-177-431-8
Search completed: April 18, 2005, 08:18:36
Job time : 18.4745 secs
                                                                                     밁
                                                                                                                                                                      Query Match 74.1%;
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
FILING DATE:
APPLICATION NUMBER: 08/955,472
FILING DATE:
APPLICATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/050001
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/542-9806
TELEPX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6071700
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-9806
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 971 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSEE: Fish & Richardson P.C.
ADDRESSEE: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPRETIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 F.
CITY: Boston
STATE: MA
                                                                                     726 iGVITPYEGO 735
                                                                                                                1 IGVITPYXXQ 10
                                                                                                                                                                      Score 40; DB 3; Length 971; Pred. No. 8.1; 0; Mismatches 2; Indels
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lorden mold abod sint

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                           Regult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
Query
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)U80\(\Bar{B}\) PUBCOMB\(\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\) U80\(\Bar{B}\) PUBCOMB\(\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\) U81\(\Bar{B}\) PUBCOMB\(\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\) U81\(\Bar{B}\) PUBCOMB\(\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\) U81\(\Bar{B}\) PUBCOMB\(\Bar{B}\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\) U81\(\Bar{B}\) PUB\(\Bar{B}\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)/\(\)/\(\)(\) PUB\(\Bar{B}\). PUB\(\Bar{B}\) pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\) pubpaa\(\)/\(\)(\)3\(\)\(\)\(\)\\ n\(\Bar{B}\) PUB\(\Bar{B}\). pep\(\):\*
n\(\bar{Z}_{\}\) ptodata\(\)/\(\)\(\) pubpaa\(\)/\(\)\(\)\(\)\(\)\(\)\\
n\(\Bar{B}\). PUB\(\Bar{B}\). PUB\(\Bar{B}\). PuB\(\Bar{B}\).
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6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                                                                                        SUMMARIES
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13	12	11	10	9	6	7	0	ហ	4	ω	N	P	No.
44	45	45	46	46	46	47	47	47	47	47	47	47	Score
81.5	83.3	83.3	85.2	85.2	85.2	87.0	87.0	87.0	87.0	87.0	87.0	87.0	Match
69	317	182	1944	648	14	642	639	637	626	404	332	127	Match Length DB ID
16	15	16	15	15	16	15	15	15	16	15	15	16	DB
US-10-437-963-106566	US-10-425-114-42716	US-10-767-701-62775	US-10-369-493-2521	US-10-369-493-21357	US-10-652-334-7	US-10-425-114-37557	US-10-425-114-37717	US-10-424-599-233501	US-10-437-963-166322	US-10-425-114-37833	US-10-425-114-38637	US-10-767-701-48804	ID
Sequence 106566,	Sequence 42716, A	Sequence 62775, A	Sequence 2521, Ap	Sequence 21357, A	Sequence 7, Appli	Sequence 37557, A	Sequence 37717, A	Sequence 233501,	Sequence 166322,	Sequence 37833, A	Sequence 38637, A	Sequence 48804, A	Description

RESULT 2

40	40		40	40	40 40 74.1	39 40 74.1		74.	41	41 75.		42	79.				43 79.	44 81.	44	44	44	44 81.	81.	44 81.	20 44 81.5	44 81.	44 81.	44	44 81.	
638	380	350	312	215	199	172	142	50	237	219	10	415	2646	1361	650	642	250	1975	1349	1211	1208	1187	959	804	683	550	517	417	414	
16	16	15	15	15	16	15	15	ø	15	16	16	16	16	16	5	15	15	16	14	9	14		16	5	15	14	14	15	16	
US-10-437-963-181690	US-10-652-334-29	US-10-424-599-241211		US-10-425-114-42518	US-10-767-701-38822	US-10-424-599-278250	US-10-335-977-8637	US-09-864-761-38825	US-10-424-599-202249	US-10-767-701-57601	US-10-652-334-11	US-10-652-334-25	US-10-437-963-189923	US-10-437-963-165703	US-10-369-493-2884	US-10-369-493-21526	US-10-424-599-259854	US-10-437-963-140079	US-10-077-583-6	US-09-801-574-60	US-10-077-583-4	US-09-801-574-14	US-10-437-963-123484	US-10-104-047-3161	US-10-369-493-22264	N	US-10-077-583-8	US-10-116-275-139	US-10-652-334-28	
Sequence 181690,	Sequence 29, Appl	241	Sequence 45797, A	Sequence 42518, A	38822,	Sequence 278250,	Sequence 8637, Ap	38825,	Sequence 202249,	5760	Sequence 11, Appl	Sequence 25, Appl	1899			Sequence 21526, A	Sequence 259854,		6,		•	Sequence 14, Appl	12:		22			139		,

ALIGNMENTS

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                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB3476-013-P1-K1-B11.pep US-10-767-701-48804
                                                                                                                                                                                                                                                                                                   APPLICANT: KOVAIC, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILB REFERENCE: 38-21(5335)B
CURRENT PLICATION NUMBER: US/10/767,701
CURRENT PLIING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 48804
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-767-701-48804
                                                                    Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48804, Application US/10767701 Publication No. US20040172684A1
                                                                                                                                                                           FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(127)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Sorghum bicolor
15
                                  1 IGVITPYXXQVXXL 14
                                                                      9;
                                                                                       Similarity
IGIITPYSAQVICL 28
                                                                    Conservative
                                                                                       87.0%;
                                                                      Score 47; DB 1
Pred. No. 0.15;
1; Mismatches
                                                                                                          DB 16; Length 127;
                                                                        Indels
                                                                      0,
                                                                        Gaps
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US-10-437-963-166322

Sequence 166322, Application US/10437963

Publication No. US20040123343A1

; GENERAL INFORMATION:
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                                                                                       RESULT 4
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                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 37833
LENGTH: 404
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Matches 9; Conserv
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SEQ ID NO 38637
LENGTH: 332
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                      Query Match
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APPLICANT:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                     Local
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                                                                                                                                             292
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9; Conserv
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Screen, Steven E
Tabaska, Jack E
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Screen, Steven E
Tabaska, Jack E
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                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                   87.0%;
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64.3%;
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                                                                                                                                                                                                                                   Score 47; DB 15; Length 404; Pred. No. 0.51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
TYPE: PPT
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                                                                                                                                 ; OTHER INFORMATION: Clone ID: US-10-424-599-233501
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                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233501
                                                                 Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 233501, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OP INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                LOCATION: (1)..(637)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                 NAME/KEY: unsure
                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(626)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
                                                                                                                                                                                                                                                                                     ENGTH: 637
                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 9; Conserv
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515 IGIITPYAAQVTCL 528
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                               1 IGVITPYXXQVXXL 14
                                                                Similarity 64.: 9; Conservative
IGIITPYAAQVVLL 538
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Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                 87.0%;
                                                                                                                                               PAT_MRT3847_52878C.1.pep
                                                                               Score 47;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 16; Length 626; Pred. No. 0.81;
                                                                                   0.82;
                                                                                                DB 15;
                                                                                               Length 637;
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                                                                Gaps
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US-10-425-114-37717; Sequence 37717, Application US/10425114

RESULT 6

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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwel

TITLE OP INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement

PILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 37557

LENGTH: 642

TYPE: PRT
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Best Local Similarity
""" hes 9; Conserva
                                                                                                                     US-10-652-334-7
                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB3170-056-H12_FLI.pep US-10-425-114-37717
                                                            GENERAL INFORMATION
                                                                            Sequence 7, Application US/10652334 Publication No. US20040115787A1
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SEQ ID NO 37717
LENGTH: 639
APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                              531 IGIITPYAAQVMLL 544
                                                                                                                                                                                                                                    1 IGVITPYXXQVXXL 14
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                             87.0%;
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64.3%;
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Pred. No. 0.83;
1; Mismatches
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    Mismatches

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US-10-369-493-2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-10-369-493-21357
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US-10-369-493-21357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21357
LENGTH: 648
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                            Sequence 2521, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Best Local Similarity
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT PEPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR PILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 601-1-65N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14
TYPE: PRT
ORGANISM: Baccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                   85.2%;
Local Similarity 71.4%;
es 10; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB
Pred. No. 1.3;
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0.023;
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US-10-767-701-62775
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; LENGTH: 1944
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-767-701-62775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 62775
LENGTH: 182
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42716
LENGTH: 317
                                                                                                                                                                                                                                                                                                               Sequence 42716, Application US/10425114 Publication No. US20040034888A1
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        -10-425-114-42716
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                                                                                                APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                            CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PLANTS WITH IMPROVED FILE REFERENCE: 38-10 (52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: 18065480.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 83.3%;
Local Similarity 64.3%;
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; Pred. No. 4.3;
1; Mismatches
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Pred. No. 0.55;
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FILE REFERENCE: H1-A0105
CURRENT FILING DATE: 202-03-25
CURRENT FILING DATE: 202-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2090
LENGTH: 125
Query Match
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                                                                                                                                                                                                                                                                                       Sequence 2090, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

APPLICANT: HELIX NO. US20030236392A1el full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-0:
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 106566
LENGTH: 69
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                    LENGTH: 12
TYPE: PRT
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Wu, Wei
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Pred. No. 0.31;
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ALIGNMENTS

RESULT 1

T02699

probable helicase At2g03270 [imported] - Arabidopsis thaliana
probable helicase At2g03270 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T18E12.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02699; D84446
C;Accession: T02699; D84446

R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, September 1998 A;Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.

A;Molecule type: DNA A;Residues: 1-635 <ROU> A;Cross-references: UNIPROT:O81047; EMBL:AC005313; NID:g3548797; PID:g3548803

A;Status: translated from GB/EMBL/DDBJ

A; Reference number: Z14702 A; Accession: T02699

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
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A;Map position: 2
C;Superfamily: probable DNA helicase MJ0104
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A; Residues: 1-635 <STO>
                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                       Local Similarity les 9; Conserv
                                                                                                                                                                                                                    524
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                                                                                                                                                                                                                  IGIITPYAAQVMLL 537
                                                                                                                                                                                                                                                     IGVITPYXXQVXXL 14
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                       87.0%;
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                                                                                                                                                                                                                                                                                                             No.
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B.; Umayam, L.; Tallon, L.:
                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                          Gaps
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sysmith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tRNA-splicing endonuclease positive effector - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                          á
                                                                                                                                                                                                                                                                                                                                        R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, November 1999
A;Reference number: Z22230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T40065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-648 < KLB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-678 < AAA>
                                                                                                                                                                                                                                                                                                                         A;Reference number:
A;Accession: T42668
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DKFZp434B0717.1 - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number:
A;Accession: T40065
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A;Residues: 1-1944 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                       ;Cross-references: UNIPROT:Q9BXT6; EMBL:AL133068
                                                                                                                                                                                                                                                                                                   ;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                        ;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004;Accession: T42668
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;Experimental source: strain 972h-; cosmid c29Al0
                                                                                            Matches
                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                  Experimental
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Best Local
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            530
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Similarity 64.3%;
9; Conservation
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Similarity 71.4%;
                                                                                                               Similarity
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IGVITPYRKQV 540
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                                                   IGVITPYXXQV 11
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                                                                                            Conservative
                                                                                                                                                                                                                    adult testis;
                                                                                                             81.5%;
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Pred. No. 0.5
1; Mismatches
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Pred. No. 0.17;
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Pred. No. 0.
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0.57;
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R;Rieger, M.
submitted to the Protein Sequence Database,
A·Reference number: S37832
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S34700; S37830; S37834
R;Wieman, S; Voss, H; Schwagaer, C; Rupp, T; Stegemann, J; Zimmermann, J; Grothue submitted to the EMBL Data Library, July 1993
A;Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome A;Reference number: S34679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S34700
                                                                           A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwart, Shinn, P.; Southwick, A.M.; & ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                               R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
C86189
                                                                                                                                                                                                                                                                                                                                                                                                                               protein T25N20.11 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable purine nucleotide-binding protein YKL017c - yeast (Saccharomyces cerevisiae)
С;Species: Saccharomyces cerevisiae
A; Molecule type:
                         A;Status: preliminary
                                                     A; Reference number: A86141; A; Accession: C86189
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A;Cross-references: EMBL:Z28017; NID:g486006; PID:g486007; MIPS:YKL017c
A;Experimental source: strain S288C
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A;Experimental source: strain S288C
R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp
submitted to the Protein Sequence Database,
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Best Local Similarity
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L; Mismatches
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Pred. No. 0.48;
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                                                                                                                                                                                                                                                                                                                       C.J.; Federspiel, N.A.; Conway, A.B.; Conway, A.
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                                                                                                                                                             P.; Southwick, A.M.; Sun,
                                                                                                                                                                                                                                                                                                                            iel, N.A.; Kaul, S.; WI
Conway, A.R.; Creasy,
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                                                                                                                                                                                                                  S.; Khaykin, E.; Kim, S.; Maiti, R.; Marzia
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                                                                                                                                                                                                                                                                                                                               S.; White, (reasy, T.H.;
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;Cross-references: UNIPROT:Q9LR48;

GB:AE005172; NID:g8778728; PIDN:AAF79736.1;

GSPDB:GN

1-1048 <STO>

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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: D72258
RESULT
D69085
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                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Gene: T25N20.11
A;Map position: 1
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A;Experimental source: strain 972h-; cosmid c6G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, submitted to the EMBL Data Library, August 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1687 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T39072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z21825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                     Molecule type: ARN's Residues: 1-245 ARN's Cross-references: UNIPROT:Q9X1D1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Schizosaccharomyces pombe;Date: 03-Dec-1999 #text_change 09-Jul-2004;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                             Best
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: SPDB:SPAC6G9.010c
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                                                                                                                                          Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 81.5%;
Similarity 64.3%;
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9; Conserva
                                                                        IGIITPYDDQV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||| |: |
|GVITPYRSQLHEL 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGVITPYRQQV 765
                                                                                                       IGVITPYXXQV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGVITPYXXQVXXL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGVITPYXXQV 11
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family protein - fission yeast (Schizosaccharomyces
                                                                                                                                                         79.6%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2;
Pred. No. 1.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0:
                                                                                                                                        Score 43; DB 2
Pred. No. 0.26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                   GB:AE001793; GB:AE000512; NID:G4981963; PIDN:AAD364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                          DB 2;
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                                                                                                                                                                          Length 245;
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                               A; Reference number: Z26053
A; Accession: T52521
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G72429
              A; Status: preliminary
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C;Genetics:
A;Gene: TM0005
C;Superfamily: probable DNA helicase MJ0104
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72429
R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                    C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision
                                                                                                                                                                                        related to SEN1 protein [imported] - Neurospora crassa
N;Alternate names: protein B2J23.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea
A;Reference number: A72200; MUID:99287316; PMID:10360571
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C;Accession: D6985
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzboweki, J.; Gibson, R.; Jiwani, i Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzboweki, J.; Gibson, R.; Jiwani, i Qiu, D.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, P.; Noe
                                                                                C;Accession: T52521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9WXM0; GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD3509·
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-650 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: G72429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription control factor enhancer-binding protein - Methanobacterium thermoautotroph
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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C;Superfamily: probable DNA helicase MJ0104
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Best Local Similarity
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Aign, V.; Hoheisel, J.; Bran
ne Protein Sequence Database,
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72.7%;
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Pred. No.
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Pred. No. 0.73;
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Brandt, P.; Fa:
base, September
                                                                                                        20-Oct-2000 #text_change
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พ
    Fartmann, B.; Holland, R.;
ber 2000
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C;Accession: D86303
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. Aller, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; A;Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1825 <SCH>
A;Cross-references: UNIPROT:(9HFI5; EMBL:AL442164; GSPDB:GN00116; NCSP:B2J23.170
A:Rxnerimental source: BAC clone B2J23; strain OR74A
                                                                                                                                                                                                                                                            R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                          D90303
hypothetical protein SSO1456 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-139 <KUR>
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A;Accession: D90303
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A;Residues: 1-2142 <STO>
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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2; Mismatches
        Score 42; DB
Pred. No. 0.23
2; Mismatches
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A;Residues: 1-530 -AAGF>
A;Cross-references: UNIPROT:067840; GB:AE000770; NID:g2984274; PIDN:AAC07803.1; PID:g2984
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AT4g05540 [imported] - Arabidopsis thallana
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
Search completed: April 18, 2005, Job time : 13.4891 secs
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A; Accession: F85069
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;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                     ;Cross-references:
                                                                                                                                                                                                                                                                                                                                                           Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana;Reference number: A85001; MUID:20083488; PMID:10617198
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US-10-652-334-7 54 1 IGVITPYXXQVXXL

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Scoring table:

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O6589 drosophila
Q9fgv0 arabidopsis
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Q9bxt6 homo sapien
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O27671 methanobact
O6cfh6 yarrowia li
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O6cfh6 yarrowia li
O9wxm0 thermotoga
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C TISSUE=Whole plant;
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Ma repressor with similarities to pro- and eukaryotic DNA
T "A repressor with similarities to pro- and eukaryotic DNA
T controls the assembly of the CAAT-box binding complex at ;
photosynthesis gene promocear.";
J J Biol. Chem. 10:1074(2001).

E MBL; AJ300306; CAC16347.1; -.

R GO; GO:0003577; F:DNA binding; IEA.
R GO; GO:0003677; F:DNA binding; IEA.
R GO; GO:0003677; F:DNA binding; IEA.
R GO; GO:000486; F:nucleotide binding; IEA.
R GO; GO:000486; F:nucleotide binding; IEA.
R InterPro; IPR001593; AAA ATPase.
R InterPro; IPR001593; AAA ATPase.
R InterPro; IPR004483; put_DNA_helic.
R SMART; SM00487; DEXDC; 1.
R SMART; SM00487; DEXDC; 1.
R TIGRERMS; TIGR0376; put_DNA_helic; 1.
W ATP-binding; Helicase.

SEQUENCE 635 AA; 70335 MW; 6149646686631F29 CRC64;
O81047 PRELIMINARY;
O81047, Q94AT0;
O1-NOV-1998 (TrEMBLrel. 08
O1-JUN-2002 (TrEMBLrel. 21
O5-JUL-2004 (TrEMBLrel. 27
Putative helicase.
Name=At2g03270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FNX9 PRELIMINARY;
Q9FNX9;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2004 (TrEMBLrel. 26, L
Puttative helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=atpc-2 gene;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                N
                                                                                                                                     524
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                                                                                                                                                                                    Similarity 64.: 9; Conservative
                                                                                                                                  IGVITPYXXQVXXL
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660
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967
1121
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Q9S9W3
QBEDR3
QBEASO
YEOG YEAST
QBAOG7
QBAOG7
QGAXY7
YHR ECOLI
Q9ALG4
QBSYL13
Q74ZU0
Q9SHX6
Q9SHX6
Q9SHX6
Q9SHX6
Q9SHX6
                        Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation updat
                                                                                                                                                                                               Score 47; DB 2;
Pred. No. 0.61;
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                                                                                                                                                                                     Mismatches
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Q829w3
Q8rdr3
Q86880
Q82644
Q8207
Q64xy7
Q64xy7
P39369
Q98164
Q88vi3
Q74xu0
Q98hx8
O64476
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Result No.

Score

Query Match

Length

BB

773996666655

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Gape

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RESULT
Q6F2U8
ID Q6
AC Q6
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QA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

QA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.

QA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

QA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

QA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

QA Kamiya A., Echen H., Narusaka M., Nguyen M., Palm C.J.,

QA Meyers M.C., Miranda M., Marusaka M., Nguyen M., Palm C.J.,

QA Meyers M.C., Miranda M., Shinn P., Southwick A., Shinozaki K.

QA Davis R. W., Ecker J.R., Theologis A.;

QA BEBL; ACO05213; AAM15033.1; -.

QA BEBL; AY045820; AAK76494.1; -.

QA BEBL; AY091361; AAM14300.1; -.
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Best Loc
Matches
  Q6F2U8;
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Goldemith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bo
Carminci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003593; AAA ATPase.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR004483; put_DNA_helic.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR00376; put_DNA_helic; ATP-binding; Helicase.
SEQUENCE 639 AA; 70850 MW; C913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
Kaul S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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                                                                                  w
                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0004386; F:helicase activity; GO:0000166; F:nucleotide binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; T02699; T02699.
GO:0005524; F:ATP binding; IEA.
GO:0003677; F:DNA binding; IEA.
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y S.D., Lin X., 1
, Ronning C.M., 1
ed (MAR-2000) to
                                                                                                                                                                                                                                                                        Similarity
9; Conser
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                                 PRELIMINARY;
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64.3%;
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                                                                                                                                                                                                                                                                                                 Score 47;
Pred. No.
                                 PRT;
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                                                                                                                                                                                                                                                                           Mismatches
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A., Ronning C.,
C.D., Y
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J C.M., Be
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Jones
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, Bowser L.,
J., Jones T.,
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Ecker J.R.,
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RESULT
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Best Local
STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Kerchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D. Ketchum K.A., Dodson R.J., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.I. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A., Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
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028883;
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Oryza sativa (japonica cultivar-group).
Cutyas sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA helicase, putative.
OrderedLocusNames=AF1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00376; put_DNA_helic; ATP-binding; Helicase. SEQUENCE 651 AA; 71304 MW; EC70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2004) to the EMBL/Geni
EMBL, AC133003; AAT76339.1; -.
EMBL; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004386; F:helicase activity;
GO; GO:0004386; F:helicase activity;
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25-OCT-2004 (TrEMBLrel.
Putative DNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Archaeog
Archaeoglobaceae; Archaeoglobus
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InterPro; IPR011545;
InterPro; IPR004483;
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25-OCT-2004
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SM00487; DEXDc;
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DEAD/DEAH_1
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB Pred. No. 0.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EC701B00C45E8ED9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence up
annotation
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; IEA
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                                                                                                                                                                                                                                  Peterson J.D.,
                                                                                                                                                                                 Gill S.R.,
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                                                                                                                                                  в.J.,
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ALD SERVICE SERVICES 
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Query Match
Best Local Similarity
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Best I
                                                                                                                    InterPro; IPR004483; put_DNA_helic.
InterPro; IPR001374; R3H.
InterPro; IPR00058; Znf_AN1.
InterPro; IPR000058; Znf_AN1.
InterPro; IPR000058; A3H; 1.
SMART; SM00382; A3H; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00393; R3H; 1.
INTERPAMS; TIGR00376; put_DNA_helic; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q75JA0;
                                                                           TIGRFAMS; TI
ATP-binding.
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22092622; PubMed-12097910; DOI-10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001009; ABAB9860.1; -.
PIR; C69423; C69423.
TIGR; AP1388; -.
                                                                                                                                                                                                                                                                                                                                                                                                     និនិនិ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostellum discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to Rattus norvegicus (Rat). Antifreeze-enhancer binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMs; TIGR00376; put DNA_helic; 1.
ATP-binding; Complete proteome; Helicase.
SEQUENCE 648 AA; 73775 MW; B5074507DN
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA_ATPAse.
InterPro; IPR011545; DEAD/DEAH_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004386; F:helicase activity; I
GO; GO:00001.66; F:nucleotide binding;
InterPro; IPR003593; AAA ATPase.
InterPro; IPR004483; put_DNA_helic.
SMART. SMONG182: AAA. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
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                                                                                                                                                                                                                                                                                                                                                                                                mitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
L; ACT17072; AAS38931.1; -.
GO:0005524; F;ATP binding; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0000166; F:DNCleotide binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nce and analysis of chromosome 2 418:79-85(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGVITPYDDQVDLL 550
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                                                                             1024
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                                                                           AA;
                                                                                                                  put_DNA_helic; 1.
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71.4%;
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  Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                             92352F4C44885C5A CRC64;
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                         Length 1024;
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RA Sgouros J., Peat N., Hayles J., Bakar S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C., RA Collins M., Connor R., Cronin A., Davis P., Peltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C., RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C., RA RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Rohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA, Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., RMBL, ALIJ34453 Char7470 1.
RESULT 7
ARMI_DROME
ID ARMI_D
AC Q6J5K9
DT 25-OCT
DT 25-OCT
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094387
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                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                GeneDB SPombe; SPBC29A10.10c;
InterPro; IPR000873; AMP-bind.
PROSITE; PS00455; AMP BINDING;
SEQUENCE 1944 AA; 222209 MW
                                                                                                                                                                                                                                                                                                                                 EMBL; AL034463; CAA22438.1; PIR; T40065; T40065.
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Name=SPBC29A10.10c;
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01-MAY-1999 (TrEMBLrel. 10,
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                                                                                                                                                                                                Similarity 9; Conserv
                                                                                                                               IGVVTPYRSQVQQL 1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11859360; DOI=10.1038/nature724;
R., Rajandream M.A., Lyne M., Lyne R.,
N., Hayles J., Baker S., Basham D., Bowm
                                                                                                                                                                                                               85.2%;
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26,
                                                                                                                                                                                                                                                                   MW;
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Last annotation update)
                                                                                                                                                                                                  Score 46; DB
Pred. No. 2.8;
1; Mismatches
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2.8;
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ARMI DROME STANDARD; 05J5K9; 09VZP4; 25-OCT-2004 (Rel. 45, Created) 25-OCT-2004 (Rel. 45, Last seq

sequence update)

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RX MEDLINE-2019606; pubMed=10731132; DOT=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Walson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barndon R.C., Benos P.V., Bernan B.P., Bhandaari D., Bolshakov S., Ra Beeson K.Y., Benos P.V., Bernan B.P., Bhandaari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Brottler P., Ra Borkova D., Botchan M.R., Downes M., Dugan Rocha S., Davies P., Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foeler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Ra Hostin D., Houtton K.A., Howland T.J., Wei M.-H. Deynam C., Ra Hostin D., Roston E., Mandar J., Li J., Liang Y., Lin X., Liako Y., Lin X., Mathel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Kramel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mandari M., Wei M., Mandar J., Wei M., Melson D.L., Mclich H., Liako P., Liang Y., Lin X., Liako P., Liang Y., Lin X., Liako P., Liako P., Liako P., Liako P., Mandar J., Wei M.,
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TISSUE=OVATY;
PubMed=1500
                                                                                                                                                                                  MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
systematic review. Genome Biol. 3:RES [4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENOME REANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 116:817-829(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15035984; DOI=10.1016/S0092-8674(04)00250-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2005 (Rel.
                                                                                                                                                              S.B.;
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                                         3:RESEARCH0083.1-RESEARCH0083.22(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
armi (EC 3.6.1.-) (Armi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Armitage protein)
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IGVITPYXXQVXXL 14

Best Loc Matches Query Match

Local

Similarity 9; Conserv

Conservative

83.3%; 64.3%;

Score 45; Pred. No. Mismatches

BB

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Length 1274;

Indels

<u>.</u>,

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SEQUENCE

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C340E2B5E4F75653

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Expressed at low level throughout development, including somatic tissues. First apparent early in oogenesis, in the cytoplasm of stem cells and mitotically dividing cystoblasts. In regions 2a and 2b of the germarium, it is most concentrated in the center of the germline cysts, where the pro-oocyte is located. In stage 1 and early stage 2 egg chambers, it accumulates at the anterior of the cocyte, near the ring canals. It also extends through the ring canals forming a branched structure that links the early oocyte with adjacent nurse cells. In stage 3 cysts, it accumulates at the posterior cortex and localizes to extensions that pass through the cocyte into the nurse cells. Through stages 4 to 7, it continues to be somewhat enriched at the posterior cortex of the oocyte, but at significantly lower level. In stage 9 to 10 egg chambers, it is found throughout the cytoplasm of the oocyte and nurse cells, with slight enrichment at the oocyte cortex.

SIMILARITY: Belongs to the DNA2/NAM7 helicase family. SDE3
                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomari Y., Du T., Haley B., Schwarz D.S., Bennett R., Cook H.A.,

Koppetsch B.S., Theurkauf W.E., Zamore P.D.;

"RISC assembly defects in the Drosophila RNAi mutant armitage.";

Cell 116:831.841(2004).

-I- FUNCTION: Probable RNA helicase required for axial polarization of
the occyte during early and mid cogenesis. Plays a central role in
RNA interference (RNAi) process, a process that mediates mRNA
destruction of translational repression. Required for the assembly
of the RISC complex, a complex required for target RNA destruction
or repression. May be required in the RISC assembly to unwind
miRNAs, in the production of single-stranded miRNA from the
double-stranded miRNA, a key step in RISC formation. Required both
for the translational control of oskar (osk) mRNA and cytoskeletal
                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                     CONFLICT
                                                                                         VARSPLIC
                                                                                                                                                                                                                   FlyBase; FBgn0041164; armi.
                                                                                                                           VARSPLIC
                                                                                                                                                                                  Hydrolase.
                                                                                                                                                                                                   Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15035985; DOI=10.1016/S0092-8674(04)00218-1;
                                                                                                                                                                   BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polarization in the occyte.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
                                                                                                                                                                                                                                                           AE003478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note=No
                                                                                                                                                                                                                                                                            AY598469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q6J5K9-1; Sequence=Displayed;
Note=No experimental confirmation a
608
613
991
1274
                                                                                                                                                                                                 splicing; ATP-binding; Developmental protein; Helicase;
                                                                                         87
                                                                                                                                                                                                                                                         AAF47775.1; -.
                                    608
613
                                                                                                                           98
951
918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abundant in
               DEAG box (By similarity).

Missing (in isoform B).

/FIId=VSP_011795.

DKKAAH -> MTYVS (in isoform B)

/FIId=VSP_011796.

T -> V (in Ref. 1).

I -> V (in Ref. 1).

S -> L (in Ref. 1).
                                                                                                                                                                   (Potential)
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                                                                                                                                                                                                                                                                                                                                                               There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                      restrictions
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RESULT 9
Q75CL7
ID Q75CL7
O75C
AC Q75C
AC Q75C
DT 05-J
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Best Local
                                                              AGD; ACL098C;

GO; GO:0003572; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0000166; F:nucleotide binding; II
InterPro; IPR003593; AAA ATPASS.
InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR004483; Dut DNA helic.
InterPro; IPR00212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
SMART; SM00382; AAA; 1.
SMART; SM00387; DEXDC; 1.
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Q9FGV0;
01-MAR-2001 (TrEMBLrel. 16, 0
01-MAR-2001 (TrEMBLrel. 16, 1
01-MAR-2001 (TrEMBLrel. 16, 1
Gb|AAD48967.1.
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Q75CL7;
05-JUL-2004
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVN Res. 7:31-63(2000)
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ATP-binding.
                                                                                                                                                                                                                                                                                                                           EMBL; AE016816; AAS51130.1;
                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 10895;
Brachat S., Voegeli S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=ACL098C;
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                                                  TIGRFAMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                             TIGR00376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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60456 MW;
  72946 MW;
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57.1%;
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27,
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                                                                                                                                                                                                                                                                                                                                                                                               Dietrich F.S., Lerch A., Gaffney T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Last annotation update)
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Pred. No.
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    2BC1905117D6DC2A
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                                                                                                                                                                                                                                    IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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Matches
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Q6CMS
AC AC Q6CMS
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                                                                                                             Matches
                                                                                                                                    Query Match
Best Local
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Best Local 9
                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA ATPABE.
InterPro; IPR011545; DRAD/DRAH N.
InterPro; IPR014483; DUL DNA helic.
InterPro; IPR004212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dujon B. Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bloykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre B., Falrhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6CMS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382125; CAG99853.1; -.
EON GO:0005524; F:RAFP binding; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0003867; F:helicase activity; IEA.
GO; GO:0004386; F:nucleotide binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
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                                                                                                                                                                                                                                                 ATP-binding;
                                                                                                                                                                                                                                                                             TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bouchier C., Caudron B., Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames=KLLA0E18150g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to sp P34243 Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=284590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis NRRL Y-1140.
565
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                                                                                                             9,
                                                                                                                                      Similarity
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IGVISPYNSQVSLL 578
                                                IGVITPYXXQVXXL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGVITPYXXQVXXL
                                                                                                                                                                                                                                           TIGR00376; put_DNA_helic;
                                                                                                                                                                                                                       681 AA;
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                       77155 MW; D3878209DCEF6377 CRC64;
                                                                                                                                    81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.5%;
64.3%;
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Last annotation update)
romyces cerevisiae YKL017c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                          Score 44; DB 2;
Pred. No. 2.7;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB Pred. No. 2.6;
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                                                                                                             4.
                                                                                                                                                           Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetes;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIP1
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RESULT 12
SDE3 ARATH
ID SDE3 A
AC Q8GYD9
DT 25-OCT
DT 25-OCT
DT 25-OCT
DE Probab
DE 3).
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                           SDE3 ARATH
Q8GYD9; Q94KS
25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
Probable RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S000001500; H/S1.
GO; GO:0005658; C:alpha DNA polymerase:primase complex; IPI.
GO; GO:0003678; F:DNA helicase activity; IDA.
GO; GO:0006273; P:lagging strand elongation; IPI.
InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR001483; put_DNA_helic.
SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
SMART; SM00382; DEXDC; 1.
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YKB7 YEAST
P34243;
  Probable
3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X74152; CAA52266.1; -. EMBL; Z28017; CAA81852.1; -. PIR; S34700; S34700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1994 (Rel. 28, Last seq
05-JUL-2004 (Rel. 44, Last ann
Hypothetical 78.3 kDa protein
OrderedLocusNames=YKL017C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieger M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0376; put_DNA helic; 1.
ATP-binding; Helicase; Hypothetical protein.
NP_BIND 229 236 ATP (Potential).
SEQUENCE 683 AA; 78272 MW; FCD02680757377B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GermOnline; 139773; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=94205264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharon Saccharon Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequencing and analysis of 51.6 kilobases on the left arm of chromosome XI from Saccharomyces cerevisiae reveals 23 open reframes including the FAS1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                  Q94KS1; Q9LR48;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 9; Conser
                                                                                                                                                                                                                                                                                                   IGVISPYNAQVSHL 582
                                                                                                                                                                                                                                                                                                                                                        IGVITPYXXQVXXL 14
                                                    (Rel. 45,
(Rel. 45,
(Rel. 45,
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                 helicase
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%;
64.3%;
                              Last sequence update)
Last annotation update)
SDE3 (EC 3.6.1.-) (Sile
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Last annotation update)
protein in RAM2-ATP7 in
                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; D
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycotina; Sacchcetaceae; Saccharomyces.
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                 1002
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Erfle H., Hew
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
2.7;
                              (Silencing defective
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                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                              protein
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RC STRAIN-CV. Columbia;

RX MEDLINB-CV. Columbia;

RM Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rh Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rh Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rh White O., Alonso J., Altafi H., Araujo K., Booman C.L., Brooks S.Y.,

Rh Muhite O., Alonso J., Altafi H., Araujo K., Booman C.L., Brooks S.Y.,

Rh Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Rh Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Rh Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Rh Chung M.K., Conn L., Conway A.B., Cronway A.R., Fong B., Fujii C.Y.,

Rh Chung M.K., Conn L., Hass B., Hansen N.F., Hughes B., Huizar L.,

Rh Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

Rh Hunter J.L., Jenkins J., Johnson-Hoson C., Khan S., Khaykin E.,

Rh Hunter J.L., Jenkins J., Johnson-Hoson C., Khan S., Khaykin E.,

Rh Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Rh Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Rh Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Rh Miltscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,

Rh Aid, R., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

Rh Asia G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

Rh Asia G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

Rh Asia G., Peterson J., Pham P. K., Rizzo M., Southwick A.M.,

Rh Asia G., Peterson J., Tambunga G., Toriumi M.J., Town C.D.,

Rh Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Himber C., Dunoyer P., Moissiard G., Ritzenthaler C.,
"Transitivity-dependent and -independent cell-to-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11910074; DOI=10.1126/science.1071006;
Seki M., Narusaka M., Kamiya A., Ishida J., Satou M.,
Seki M., Rarusaka M., Kamiya A., Ishida J., Satou M.,
Nakajima M., Enju A., Akiyama K., Oono Y., Muramatsu M
Hayashizaki Y., Kawai J., Carninci P., Itoh M., Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SDE3 encodes an RNA helicase required silencing in Arabidopsis."; EMBO J. 20:2069-2078(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION. MEDLINE=21192042; PubMed=11296239; Dalmay T., Horsefield R., Braunstei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e

Spermatophyta; Magnoliophyta; eudicotyledons; core e

surosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Functional
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                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic (PI SIMILARITY: Belongs to the DNA2/NAM7
                                                                                                                                                                                                                                                                                                                                                                                                                         gene silencing (PTGS), a process that provides protection in plants against virus infection and can suppress expression of transgenes Plays a central role in RNA interference (RNAi) process, a process that mediates mRNA destruction of translational repression. Required for the assembly of the RISC complex, a complex required for target RNA destruction or repression. May be required in the RISC assembly to unwind miRNAs, in the production of single_stranded miRNA from the double-stranded miRNA, a key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OJ. 22:4523-4533(2003).
FUNCTION: Probable RNA helicase required for post-transcriptional
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in T.H., Baulcombe D.C.;
ired for post-transcriptional gene
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                    MIOL_MOUSE STANDARD; PRT; 1187 AA. Q99MV5; Q7TPA9; Q8C3WG; Q924C2; 28-PEB-2003 (Rel. 41, Created) 28-PEB-2003 (Rel. 44, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Potential helicase Mov1011 (EC 3.6.1.-) (Moloney like protein 1) (MOV10-like 1) (Cardiac helicase protein) (Cardiac-specific RNA helicase).

Name=Mov1011; Synonyms=Champ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry v
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea; Anopheles.
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA schriml I.M., Kanagina Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Godzik A., Gough J.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Secou M., Shinada K.,
RA Wilming L.G., Wymshaw-Boris A., Yansagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wymshaw-Boris A., Yansagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Mimishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Hara A., Hayashizaki Y.;
RA Hara M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN.NIH Swiss; TISSUE-Heart; MEDLINE-21290829; PubMed=11397016; DOI=10.1006/dbio. Liu Z.-P., Nakagawa O., Nakagawa M., Yanagisawa H., Richardson J.A., Srivastava D., Olson E.N.; "CHAMP, a novel cardiac-specific helicase regulated Dev. Biol. 234:497-509(2001).
                                                                                                                                                                                        PubMed=11854500; DOI=10.1073/pnas.261708699;
Liu Z.-P., Olson B.N.;
                                                                          "Suppression of proliferation and cardiomyocyte hypertrophy by CHAMP, a cardiac-specific RNA helicase.";
Proc. Natl. Acad. Sci. U.S.A. 99:2043-2048(2002).
-i-FUNCTION: Putative RNA helicase. Isoform 1 may play a role in mal germ cell development and isoform 2 may act downstream of MEF2C during heart formation. Isoform 2 acts as a cardiac-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Csm, a cardiac-specific isoform of the RNA helicase Mov
regulated by Nkx2.5 in embryonic heart.";
J. Biol. Chem. 278:28750-20757/7777
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                             Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g P.J., McCarrey J.R., Yang I
abundance of X-linked genes
. Genet. 27:422-426(2001).
               suppressor of cardiomyocyte hypertrophy and cell cycl progression, suggesting that it may suppress these puthrough the regulation of CDKNIA.
SUBCELLULAR
                                                                                                                                                                                                                                                                                             full-length cDNAs.";
420:563-573(2002).
regulation
LOCATION: 0
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ey J.R., Yang F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORM 1).
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Page D.C.;
  (isoform
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Passier R.,
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                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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GO:0005524; F:ATP binding; ISS.
GO:000287; F:magnesium ion binding; ISS.
GO:0003723; F:RNA binding; ISS.
GO:0003723; P:cell proliferation; IDA.
GO:0007517; P:muscle development; IDA.
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GO:0007283;
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1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Nkx2-5.
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: Isoform 2 expression is first observed in the linear heart tube at E8. The highest expression is in the region that will give rise to the ventricular segments. At E9.5, the ventricular expression is maintained in the looped heart tube. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and not expressed in somatic tissues tested. Isoform 2 is specific. Isoform 3 is heart specific and is specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed in caridiac myocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1891384; Mov1011
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AY303754; AAP60176.1; ALT_INIT.
AK084786; BAC39279.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF285587; AAK31966.1;
AF340211; AAK77049.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q99MV5-2; Sequence=VSP_003392;
ine=3; Synonyms=Csm, Cardiac-Berli isoform of Mov1011;
IsoId=Q99MV5-3; Sequence=VSP_010949;
SSUE SPECIFICITY: Isoform 1 Is specifically_expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q99MV5-1;
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1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; ATP-
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Pred. No. 4.6;
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DEAGQ->GGAAG: Abolishes the
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Missing (in isoform 3).
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[DN]-[GS]-Q-[SP]-I-T-[NK]-[IVN].
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RESULT 15
M10L_HUMAN
ID M10L_H
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                                 Hall R.E.,
Hunt S.E.,
                                                          MEDLINE-20057165; PubMed-10591208; DOI=10.1038/990031; Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagylley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bagylley C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Clark G., Colley D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Brans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C. Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho.S., Holmes S., Hunt C. P., Trace V. French L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Potential helicase Mov1011 (EC 3.6.1.-) (Moloney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Adipose tissue, and Cerebellu PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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"An abundance of X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21175748; PubMed=11279525; DOI=10.1038/86927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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Name=MOV10L1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BXT6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM
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Jones M.C., Kershaw J., Kimberley A.M., King A.,
, Langford C.F., Leversha M.A., Lloyd C., Lloyd I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ce of X-linked genes
27:422-426(2001).
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sue, and Cerebellum;
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expressed in spermatogonia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UGX9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1211
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RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McDaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Rammay H., Rammey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sebra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Scott C.E., Sebra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Williams L., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Winght C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Shintani A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Wang Q., Wang Y., Wang E., Water S., Hallier N., Minx P.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R., Nelson J.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA Chill, M., Walkinson P., Bodenteich A., Hartman K., Hu X.,
RA Mand A.S., Lane L., Tilahun Y., Wright H.,
RA Lane A., Shalan Y., Wang P., Wright H.,
RA Lane A., Shalan Y., Wang P., Walkinson R., Water C.E.,
RA Wang Q., Wang P., Walkinson P., Bodenteich A., Hartman K., Hu X.,
RA Pan Mand A., Shalan Y., Wang P., Walkinson R., Wang P., Walkinson R., Walkinson R., Walkinson R
                                EMBL; AP285604; AAK31983.1; -.
EMBL; AK000033; BAA90895.1; -.
EMBL; AK090740; BAC03511.1; -.
EMBL; AL034546; -; NOT ANNOTATED CDS.
EMBL; AL034546; -; NOT ANNOTATED CDS.
EMBL; AL032328; CAB63361.1; ALT SEQ.
EMBL; AL133068; CAB61391.1; -.
PIR; T42668; T42668.
Genew; HGNC:7201; MOV10L1.
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GLU-1179.
                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformat
the Buropean Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
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Submitted (
Genew; HGNC:
MIM; 605794;
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SIMILARITY: Belongs
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germ cell development.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available;
ISSUE SPECIFICITY: Isoform 1 is specifically
IMILARITY: Belongs to the DNA2/NAM7 helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9BXT6-2; Sequence=VSP_003390, VSP_003391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9BXT6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (
an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 534-1211 FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boecher M., Brandt P., Mewes H.-W., Gassenhuber J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the
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VSP_010948;
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Best Local
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                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                       Hydrolase; Polymorphism.
                                                                                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                              GO:0005622;
GO:0005524;
GO:0004004;
GO:0000287;
GO:0003723;
GO:0007281;
GO:0007281;
1063
              μ
                                       Similarity
              IGVITPYXXQV 11
                                                                                                                                                                                                                                                                                       IPR008994; Nucleic
                                                               1063
1096
1211
                                                                                               1179
                                                                                                                                                                1083
                                                                                                                                                                                1074
                                                                                                                820
                                                                                                                                               454
                                                                                                                                                                                                                                                                                splicing;
                              Conservative
                                                                                                                               650
                                                                                                                                                                                               910
                                                                                                                                                                                                                                874
                                                                                                                                                                                                                                                                                                                                        C:intracellular; IO F:ATP binding; TAS
                                                               Ş
                                                                                                                                                                                                                                                                                               P:spermatogenesis;
                                                                                                                                                                                                                                                                                                       F:RNA binding; TAS.
P:germ-cell development;
                                                                                                                                                                                                                                                                                                                      F:magnesium ion binding; TAS
                                                                        1096
                                                                               1063
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                                                                                                                820
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                                                                                                                                               454
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                                                                                                                                                                                                                902
                                                                                                                                                                                                                               875
                                       81.5%;
81.8%;
                                                                135292
                                                                                                                                                                                                                                                                                Nucleic acid OB.
ATP-binding; Developmental protein; Helicase;
                                                               MW;
                                0
                                                                                                                               /FTId=VAR_0
V -> I (in
                                       Score 44; DB
Pred. No. 4.7;
                                                                                                     /FTId=VAR_013695.
Q -> R (in dbSNP:2272837)
/FTId=VAR_013696.
                                                                                                                                                                                                       /FTId=VSP_003391.
Missing (In isoform 3).
/FTId=VSP_010945.
                                                                                                                                                                                                                               /FTId=VSP_003390
GV -> MF (in iso
                                                                                                                                                                                                                                             DEAG box.
Missing (in isoform
                                                                                      A -> E (in dbsNP:2272843)
/FTId=VAR_013697.
                                                                                                                                               Missing (In isoform 3).
/FTId=VSP_010948.
I -> L (in dbSNP:760749).
                                                                                                                                                                                /FTId=VSP_010946
EKIRILLRN -> RPA
                                                                                                                                                                                               Missing
                                                                                                                                                                       ASA=PILA/
                                Mismatches
                                                                410716BDCC85F8B1 CRC64;
                                                                                                                                                                                                                                                                (Potential).
                                                                        V (in Ref.
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                                                                                                                                        013694
                                                                                                                                dbSNP:2340601)
                                                                                                                                                                                                                                                                                                        IRP
                                                                                                                                                                                               isoform 3).
                                                                                                                                                                                RPAQARLVL
                                                                                                                                                                                                                                isoform 2).
                                               1;
                                                                                                                                                                                                                                                                                                                                 activity;
                               2
                                               Length 1211;
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                                                                                                                                                                                                                                                                                                                                  NAS
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                                Gaps
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Search Job tim time completed: April 18, 2005, 08:15:47 me : 59.4526 secs

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                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    A Geneseq_16Dec04:*
1: geneseqp1990s:*
2: geneseqp2000s:*
3: geneseqp2001s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
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103
1 VEVXTVDXFQGREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               April 18, 2005, 07:10:15; Search time 114.496 Seconds (without alignments) 77.692 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                           SUMMARIES
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Result No.	Score	Match	Length	BB	ID	Description
_	97	94.2	23	7		Abw01184
N	97	94.2	23	œ	ADP44110	Adp44110
ω	97	94.2	24	w	AAY77811	Aay77811
4	95		380	w	AAY77814	Aay77814
ű	95	92.2	380	7	ABW01205	Abw01205
6	95	92.2	380	œ	ADP44131	Adp44131
7	95	92.2	925	8	ADN19434	Adn19434
8	95	92.2	971	w	AAY98057	Aay98057
9	95	92.2	971	σ	ABR53412	Abr53412
10	95	92.2	971	7	ADK64706	Adk64706
11	94	91.3	373	œ	ADR10398	Adr10398
12	94	91.3	797	N	AAW36508	Aaw36508
13	94	91.3	935	7	ADJ69900	. Adj69900
14	94	91.3	992	8	ADS23757	Ads23757
15	94	91.3	1043	N	AAW36509	Aaw36509
16	94	91.3	1140	N	AAY21377	Aay21377
17	89	•	1118	ი	ABG73900	Abg73900
18	86	83.5	414	w	AAY77816	Aay77816
19	96		414	7	ABW01204	Abw01204
20	86		414	8	ADP44130	Adp44130
21	86		562	7	ADB63849	Adb63849
22	96		677	6	ABR82240	Abr82240
23	86	83.5	683	œ	ADS43834	Ads43834
24	86		926	8	ADQ66763	Adq66763
3	84		2	•		# LT 10010

FT FT Misc-difference FT		XX XW Modulator of ' XW Herapy; HCSB XX		SUL WOI			43 71			39 79 40 79									x ~	
<u> </u>	O O	Saccharomyces cerevisia Modulator of translation therapy; HCSB; nonsense		T 1 184 ABW01184 standard; ABW01184;			75.7		76.	9 76.7	77	77.7	79	80	9 0		80	86	20 C	80
note= "X	visiae. cation/	cerevisiae motificanslation terminonsense mutati	t entry)	peptide;		648	611	869	656	65 4 55 55	654	653	1944	2677	996	829	828	828	B 0	324
'Xaa may Unknown	Qu	ter	ت ا			00	a r	7	Φ,	20 4						4.	æ	σ,	4 4	4.
"Xaa may be any amino acid" - Unknown "Xaa may be any amino acid"	revisiae. Location/Qualifiers 1	yces cerevisiae motif viil peptime. of translation termination; MTT1; helicase HCSB; nonsense mutation; yeast.		23 AA.	ALIGNMENTS	ADS42927	AAB33009 ADS21255	ADM25464	ADN18615	ADS41904 AAB62031	AAB96566	ADS43215	ADN19868	ABR58288	AAM79295	AAM80279	ADP23318	ABR58327	AAB92977	AAB94335
		B; antiviral;					Ads21255 Ba			Ad841904 BE Aab62031 Re		Ads43215 Ba			Aam79295 Hu				Aab92977 Hu	
		ι;				Bacterial	Bacterial		Bacterial	Recombina	Putative	Bacterial	Bacterial	BCU0156 p	Human pro	Human pro	to polyp		Human pro	

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Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mtt1) in Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mtt1.
                                                                                                                                                                                                                                             /note= "Xaa may
Misc-difference 16
                 Disclosure; Col 43-44; Opp; English.
                                                                                                          Peltz S,
                                                                                                                                                                                          07-OCT-2003.
                                                                                                                                                                                                             US6630294-B1.
                                                                                       WPI; 2003-810549/76.
                                                                                                                              (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
                                                                                                                                                  22-JUL-1998;
                                                                                                                                                                     22-JUL-1999;
                                                                                                          Czaplinski K,
                                                                                                                                                   98US-0093685P.
                                                                                                                                                                      99US-00359268.
                                                                                                                                                                                                                                /label= Unknown
/note= "Xaa may
                                                                                                          Dinman JD;
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                                                                                                                                                                                                                                amino acid
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The invention relates to a method of identifying an agent that increases

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RESULT 2
ADP44110
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; beta-globin; buchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Cystic fibrosis; Novarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide
                                                                        Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTTI with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae. Synthetic.
The invention relates to a method of identifying a test composition that
                                Claim 40;
                                                                                                                                                                      Peltz
                                                                                                                                                                                                  (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
(DINM/) DINMAN J D.
                                                                                                                                                                                                                                                                                                             28-AUG-2003; 2003US-00652334.
                                                                                                                                                                                                                                                                                                                                            17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                          US2004115787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP44110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23
                                                                                                                                         WPI; 2004-449400/42
                                                                                                                                                                                                                                                                  22-JUL-1999;
                                                                                                                                                                                                                                                                               22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP44110 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast translation termination modulation protein motif VIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                              the MTT1.
                                                                                                                                                                     Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVXTVDXFQGREKDXIILSCVR
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                              SEQ ID NO
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                                                                                                                                                                                                                                                                98US-0093685P.
99US-00359268.
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Any amino acid"
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                            41pp; English
                                                                                                                                                                      Dinman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97;
Pred. No.
                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
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4e-10;
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RESULT 3
AAY77811
ID AAY7
XX AAY7
XX Moti
XX Moti
XX Moti
XX Heli
KW Heli
KW betu
XX Uni
XX U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                           New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.
                                                                                                                                                                                                                                                         Peltz S,
                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Motif VIII comprised in a gene modulating translation termination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY77811 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the amino acid sequence of the yeast protein motif VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                22-ЛП-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200005586-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulates the efficiency of translation termination comprising contacting
                                                                                                                                                                                                                                                                                                                          (UYNE-) UNIV NEW JERSEY
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                                                                                                                                                                                                                                                     Czaplinski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $
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                                                                                                                                                                                                                                                                                                                                                                                     98US-00120435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23;
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Claim 40; Page 80; 89pp; English.

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ARSULT 4
AAAY77814
ID AAY7
XX AAY7
XX YEAB
AC AAY7
AC AAY7
AC AAY7
AC AEAY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF2; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast Upf1 protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77814 standard; peptide; 380 AA
    WPI; 2000-171458/15
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                                                                                          Peltz S,
                                                                                                                                                                                    (UYNE-) UNIV NEW JERSEY.
                                                                                                                                                                                                                                                                          22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEVXTVDXFQGREXDXIILSCVR
                                                                                          Czaplinski K,
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                                                                                                                                                                                                                                                                          98US-00120435
                                                                                                                                                                                                                                                                                                                                                                    99WO-US016802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for modulating translation termination
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100.0%; Pred. No. 4.
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) I and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in pharmaceutical compositions to treat diseases associated with peptidyl pharmaceutical compositions to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a new multiprotein complex which can modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1; 89pp; English.
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CC transferase activity, especially diseases resulting from a nonsense or cc frameshift mutation e.g. beta-thalassemia, beta-globin, Duchene/Becker cc Muscular Dystrophy etc. It can be used to identify disease conditions ci involving a defect in the complex, by transfecting cells with encoding cc and after transferase activity during translation of defective complex before and after transferase activity during translation, inhibiting the peptidyl transferase activity during translation, inhibiting the complex or interaction between MTII and eRF3 or involved in enhancing translation cransisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of cranslation termination of mRNA and/or degradation of aberrant cranscripts in a cell. Agents binding to the complex can be identified care also useful to modulate the efficiency of translation in cells. They are also useful to modulate the efficiency of translation termination of compositions useful as above, and/or used to compositions modulating binding to MTII, useful to identify genes. C compositions modulating binding to MTII, useful to identify genes. C compositions have a promote degradation of aberrant compositions modulating binding to MTII, useful to identify genes. C compositions have a promote a promote degradation of aberrant compositions modulating binding to MTII, useful to identify genes. 'n

Sequence 380 AA;

\$ Matches Query Match Local l Similarity 19; Conserv VEVXTVDXFQGREKDXIILSCVR 23 Conservative 92.2%; ۲. Score 95; DB 3; 1 Pred. No. 2.2e-08; Mismatches Length 380; Indels 0 Gaps

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吊
VEVASVDAFOGREKDYIILSCVR 356
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RESULT 5
ABW01205
ID ABW0
XX ABW0
AC ABW0
XX Sacc
XX Modh
XX Hei
XX US6(
XX Sacc
XX Sa Saccharomyces Saccharomyces cerevisiae UPF1 protein ABW01205 standard; protein; 380 US6630294-B1 Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast; RENT1; HUPF1; UPF1. 15-JAN-2004 (first entry) cerevisiae

22-JUL-1998; 22-JUL-1999;

98US-0093685P 99US-00359268

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

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RESULT 6
ADP44131
ID ADP4
XX ADP4
XX ADP4
XX Yeas
AC ADP4
XX Yeas
XX Yeas
KW Yeas
KW Eran
KW Duch
KW Ovaj
KW Vovaj
XX US21
XX Sac(
XX Sac(
XX Issa
PN US21
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; peptidyl transferase modulation; beta-thalassaemia; beta-globin; Duchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Vonce, Familia Pigmentosa; Vonce, Von
                                    Identifying translation
                                                                                                                                                                                                                                                                                                (PELT/) PELTZ S.
(CZAP/) CZAPLINSKI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae UPP1 (otherwise termed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying therapy, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; translation termination; RNA helicase; MTT1;
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composition or agent,
                                                                                                                                                            WPI; 2004-449400/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2003; 2003US-00652334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peltz
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                                                                                                                                                                                                                                Czaplinski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Czaplinski K,
a test composition or agent that modulates the efficiency of termination comprises contacting the MTTI with the test or agent, and determining if the test composition or agent
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99US-00359268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoblastoma; ATM; Costmann Disease; yeast; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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82.6%;
                                                                                                                                                                                                                                ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dinman
                                                                                                                                                                                                                                        Dinman
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Pred. No. 2.2e
1; Mismatches
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2.2e-08;
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T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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밁 S

Length 380

0

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FX#X020202020202020202020202020
                                           the RNA helicase MTTI with a composition or agent under conditions compensation binding between the MTTI and the composition, detecting specific binding of the test composition or agent to the MTTI, and composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the CC composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the CC functional activity of mRNAs by altering frameshift frequency, permit committees and provide modulators (inhibitors/stimulators) of peptidyl transferase activity during initiation, elongation, termination and mRNA cogradation of translation. The agents, which may be antagonists or agonists, are useful in screening, diagnostic and therapeutic purposes, composition are useful in screening from or cause premature translation, such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular Dystrophy, Haemophilia A, Haemophilia B, Von Willebrand Disease, CC osteogenesis Imperfecta, Breast cancer, Ovarian Cancer, Wilms Tumour, in the composition of the prevent sequence represents controlesterolaemia, Retinitis Pigmentosa, or Neurofibromatosis, cc the amino acid sequence of the yeast helicase Upfl.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibits the MTT1
380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contacting
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                  cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance;
                                                                                                                                                                     Bacteria
                                                                                                                                                                                                                                                                           Bacterial polypeptide #2087.
                                                                                                                                                                                         bacterial polypeptide
                                                                                                                                                                                                                                                                                                 02-DEC-2004
                                                                                                                                                                                                                                                                                                                                        ADN19434 standard; protein; 925
                                                                                                                                                US2003233675-A1
                                                                                                                                                                                                                                                                                                                                                                                             334 VEVASVDAFQGREKDYIILSCVR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               92.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
2.2e-08;
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                                                                                                                                                                                                                                              property; ; osmosis;
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Cao Y, (CHEN/) (HINK/)

Hinkle 6J, GOLDMAN

Slater

,38

Chen

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Goldman

W 9.9 တ

18-DEC-2003

21-FEB-2002; 2002US-0360039P 20-FEB-2003; 2003US-00369493

(CAOY/)

CAO Y.

HINKLE G SLATER S CHEN X.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

WPI; 2004-061375/06

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned provide for expression of a polynucleotide encoding a polypeptide from

is positioned to

Claim 1; SEQ ID NO 2087; 122pp; English

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RESULT 9
AAY98079
ID AAY98079
XX AAY98079
XX AAY98079
XX O7-S
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX Yeas
XX Wupf3
XX Upf3
XX Upf3
XX O701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cc transformed plant having an improved property. The plant is a crop plant cc such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the crecombinant DNA construct and growing the transformed plant, where the cc polynucleotide or polypeptide is useful for improving plant with the cc improved plant properties, e.g. improved cold, heat or drought tolerance, cc increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or condition, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the growth of the printed specification or improved galactomannan cc growth of the printed specification but was obtained in electronic cc format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                    Yeast; nonsense-mediated mRNA decay pathway; NMD2; UPF1; upf1p; upf3p; gene therapy; beta-thalassmaemia; cancer; polycystic kidney disease; puchenne musicular dystrophy; Fanconi anaemia; haemophilia; hypercholesterolaemia; neurofibromatosis; Tay-Sachs disease; glycogen storage disease; cystic fibrosis; adenomatous polyposis coli; Cowden disease; Maple syrup urine disease; Wilson disease; Niemann-Pick disease; Turcot syndrome; McArdle disease; Mison disease; ornithine transcarbamylase deficiency.
                                                                                                                                                                                                                                                           Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast Upfip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 925 AA;
      20-JAN-1995;
                                                                   21-OCT-1998;
                                                                                                                                                                                               US6071700-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY98057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY98057 standard; protein; 971 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEVASVDAFQGREKDFILSCVR 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                  cerevisiae
      9508-00375300
                                                                      98US-00177431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 95; DB 8;
Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 925;
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RESULT 9
ABR53412
ID ABR5
XX ABR5
AC ABR5
AC ABR5
AX Prot
XX Mult
XX Mult
XX Mult
XX Sacc
XX Sacc
XX Sacc
XX Sacc
XX EP12
XX EP12
XX EP12
XX Baue
PI Marz
XX Babee
PI Marz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nonsense-mediated mRNA decay pathway has an important role in the CC degradation of mRNA transcripts that contain a stop codon. The products cof the UPF1 and UPF3 genes (proteins Upf1p and Upf3p, respectively) are CC essential components of this pathway. Mutations in these genes or CC inhibition of Upf1p or Upf3p function would lead to stabilisation of mRNA CC containing premature stop codons. The present sequence is the UPF1 CC protein, Upf1p, from Saccharomyces cerevisiae. The carboxy terminal of the NMD2 gene protein, Nmd2p, has been found to bind to Upf1p, leading to CC inhibition of the nonsense-mediated mRNA decay pathway. Inhibition of the nonsense mutations, e.g. breast cancer, polycystic kidney CC diseases, Niemann-pick disease, adenomatous polyposis coli, cystic CC diseases, Niemann-pick disease, adenomatous polyposis coli, cystic CC diseases, Niemann-pick disease, adenomatous polyposis coli, cystic CC glycogen storage disease, McArdla disease, polyposis coli, cystic CC diseases, Cowden disease, McArdla disease, polyposis cancer, Tay-Sachs CC disease, Cowden disease, Milson disease, polyposis kidney disease, Couchenne muscular dystrophy, adrenocortical carcinoma, Li-Fraumeni CC syndrome, Maple syrup urine disease, Turcot syndrome or beta-thalassaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                  Bauer A,
Marzioch
                                                                                                          15-MAY-2001; 2001EP-00111774
                                                                                                                                              20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                 20-NOV-2002
                                                                                                                                                                                                                                                     Saccharomyces
                                                                                                                                                                                                                                                                                                                            Protein sequence #SEQ ID 1689
                                                                                                                                                                                                                                                                                                                                                                                                   ABR53412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testing for compounds able to modulate the nonsense mediated mRNA decay pathway for increasing endogenous protein production by incubating a candidate compound with a cell having a gene with a nonsense mutation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                        Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR53412 standard; protein; 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-1997;
                                                                       (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene without mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEVXTVDXFQGREXDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           971 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVASVDAFQGREKDYIILSCVR 779
                  Gavin A, Grandi P, Krause R, F
M, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                (first entry
                                                                                                                                                                                                                                                         cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00955472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                     Kruse UD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                     Kuester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or

N-PSDB; ACC61454.

WPI; 2003-250078/25.

Disclosure; SEQ ID NO 1689; 17pp + Sequence Listing; English

relates to multiprotein complexes from

eukaryotes.

Proteins

of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM

Matches Query Match Best Local

19;

Conservative

1; Mismatches Score 95; Pred. No.

3; Indels Length 971;

0

Gaps

0

6.3e-08; DB 6;

Similarity

92.2%;

Sequence 971

AA;

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RESULT 10
ADK64706
ID ADK64
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                                                New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                Bauer A, Ga
Marzioch M,
                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                           Disease treating protein complex-derived protein #1022.
                   Disclosure; SEQ ID NO
                                                                                                                                                                                                                             27-AUG-2003.
                                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                     ADK64706;
                                                                                                                        Michon
                                                                                                                                                                                    20-DEC-2001; 2001EP-00130253.
                                                                                                                                                                                                        20-DEC-2002; 2002EP-00102902
                                                                                                                                                                                                                                                EP1338608-A2
                                                                                                                                                                                                                                                                                                                                                                        ADK64706 standard; protein;
                                                                                                                                                                (CELL-)
                                                                                         2003-638460/61.
DB; ADK64707.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                CELLZOME
                                                                                                                                                                                                                                                                                      complex;
                                       in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                          VEVASVDAFQGREKDYIILSCVR 779
                                                                                                                                 Gavin A,
M, Grandi
                                                                                                                        Leutwein
                                                                                                                                                                                                                                                                                                                                (first entry
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                                                                                                                                                                                                                                                                                      drug target; diagnosis
                                                                                                                       Superti-Furga G, Kuester B, Schultz P, Krause R, Kruse U, Merino A, Ba C, Rick J;
                  2043; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                         971 AA
                                                                                                                                  Bauch A;
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The invention relates to

novel protein complexes comprising a first

and

This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refective cDNA clones obtained by an oligo-capping method, where none of the cDNA clones of the control o

reters to

Claim 1; SEQ ID NO 3904; 2686pp; English.

New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancer

cancers.

N-PSDB; ADR08442

2004-583265/57.

Wakamatsu A, Isogai T,

ຸດຸບ

Nishikawa T, Isono Y, Nagai K, Irie R;

Sugiyama

Ħ,

Otsuki T;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                                                                                                                                                                                                                            EP1447413-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 971 AA;
                                                                                                                                                                                                                                                                                                                                           12-FEB-2004; 2004EP-00003145
                                                                                                                                                                                                                                                                                                                                                                             18-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tranquiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR10398 standard; protein; 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              second protein, or its derivative, fragment, homologue or variant.
                                                                                                                                                                                                                                                          (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 VEVASVDAFQGREKDYIILSCVR 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein useful
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                                                                                                                                                                                                        Yamamoto
A, Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 7;
Pred. No. 6.3e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. MOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated regulators of non-sense-mediated RNA decay - used to develop products for the study, diagnosis and therapy of disorders such as Marfan Syndrome, accelerated ageing and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RENT1; nonsense-mediated RNA decay; NMRD; mutation; regulator of nonsense transcripts; Marfan Syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones are identical to any known human mRNAs. describes an immunoassay to identify agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-549494/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dietz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human RENT1 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36508 standard; protein; 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9740855-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEIASVDAFQGREKDFIILSCVR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0016482P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US015769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94; DB
Pred. No. 3.2e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; therapy;
aging; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Query Match

91.3%;

Score

94;

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Length 797;

Query Match Best Local Similarity

91.3**%;** 78.3**%;**

Score Pred.

94; No.

DB 7; 9.1e-08;

Length

Sequence

935

8

Sequence 797

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This protein sequence is a fragment of the human RENT1 protein which regulates nonsense-mediated RNA decay (NMRD). This fragment of RENT1 shows homology to the yeast Upf1p protein. The RENT1 (regulator of nonsense transcripts) protein and other products can be used in the study, diagnosis and therapy of disorders involving NMRD such as Mar Syndrome, accelerated aging or various cancers

NMRD such as Marfan

Fig

18;

79pp;

English.

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RESULT 13
ADJ69900
ID ADJ69
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                                         CC altered mitochondrial function. Specifically, it refers to a method for ci identifying proteins of the human heart mitochondrial proteome that are consecutive invention describes a method for identifying proteins of the human heart mitochondrial proteome that are consecutive invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mediate, Huntington's disease, costeoarthritis, Leber's hereditary optic neuropathy (HAON), mitochondrial cencephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating the state of the sample and correlating the sample and cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial; human; screening assay; diabetes mellitus, Huntington's disease; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel mitochondrial targets that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1706; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-845369/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteopathic; ophthalmological; cytostatic
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BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fahy ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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ADS237F7
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AC ADS23
AC 
                                                                                                                                                                                                           CC The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant the having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the conditions are conditionally increased rate of the conditions are conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypoptide used in the scope of the invention. Note: The sequence data for this patent did not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 12790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microbial source, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-061375/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant DNA construct comprising a promoter positioned to provide expression of a polynucleotide encoding a polypeptide from a robial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ķ
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polypeptide
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Best Local
                                                                                                                      This sequence represents the murine RENT1 protein which regulates nonsense-mediated RNA decay (NMRD). The RENT1 (regulator of nonsense transcripts) protein and other products can be used in the study, diagnosis and therapy of disorders involving NMRD such as Marfan
                                                                                        Sequence 1043 AA;
                                                                                                             Syndrome, accelerated
                                                                                                                                                                                Claim 19; Fig
                                                                                                                                                                                                               New isolated regulators of non-sense-mediated RNA decay - used to develop products for the study, diagnosis and therapy of disorders such as Marfan
                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                       Bnw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW36509 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form part of the printed specification but was obtained in format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                     Syndrome, accelerated ageing
                                                                                                                                                                                                                                                  N-PSDB; AAT96719
                                                                                                                                                                                                                                                              WPI; 1997-549494/50.
                                                                                                                                                                                                                                                                                    Dietz HC
                                                                                                                                                                                                                                                                                                                                29-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                  WO9740855-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           RENT1; nonsense-mediated RNA decay; NMRD; mutation; diagnosis; therapy; regulator of nonsense transcripts; Marfan Syndrome; aging; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW36509
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                                                        Local
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              VEVXTVDXFQGREKDXIILSCVR 23
VEIASVDAFQGREKDFIILSCVR 766
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                                                                                                                                                                                                                                                                                                         HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 1043
                                                       91.3%;
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                                                                                                             aging or various cancers
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Match
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6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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                       VEVXTVDXFQGREKDXIILSCVR
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                   US-09-359-268A-8
US-09-359-268A-29
US-08-724-354D-4
US-09-177-431-8
US-09-270-984A-2
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US-09-270-984A-2
US-09-270-984A-2
US-09-270-984A-2
US-09-270-184A-2
US-09-270-184A-2
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US-09-248-796A-18933
US-09-270-767-47680
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1058, Ap
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32463, A
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18933, A
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US-09-359-268A-8
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	US-09-27/0-/67-59862 US-09-370-767-44429 US-09-359-268A-21 US-09-328-352-6682 US-09-939-016-8313 US-08-727-034-3 US-08-727-034-7 US-09-919-039-40 US-09-919-039-40 US-09-919-039-8648 US-09-68-947-44 US-08-68-947-44 US-08-68-373-12 US-08-479-7258-2 US-09-522-685-2 US-09-134-000C-3685 US-08-137-236-14 US-08-597-236-14	307	307	226	1833	1833	1833	500	497	142	58	2214	2214	2213	1345	1020	11	444	85
US-09-270-767-44429 US-09-329-268A-21 US-09-329-268A-21 US-09-328-352-6682 US-09-329-016-8313 US-08-727-034-7 US-08-727-034-7 US-09-19-039-4 US-09-489-039A-8648 US-09-489-039A-8648 US-09-68-947A-4 US-09-68-947A-4 US-08-68-373-12 US-08-68-373-12 US-09-68-373-12 US-09-68-373-12 US-08-479-728-2 US-08-479-728-18 US-09-134-000C-3685 US-08-59-236-14	-09-270-767-44429 -09-370-767-44429 -09-359-268A-21 -09-328-352-6682 -09-949-016-8313 -08-727-034-3 -08-727-034-7 -09-919-039-40 -09-549-441-37 -09-489-039A-648 -09-58-947A-4 -08-68-373-12 -08-479-722B-2 -08-479-722B-2 -08-479-723B-2 -08-479-723B-2 -08-479-723B-2 -08-479-723B-2 -08-486-373-12 -08-491-3685 -08-592-685-2 -08-592-685-2 -08-592-685-2 -08-592-685-2 -08-592-685-14	۳	μ	4	ហ	4.	w	ω	ω	4	4	4	_	_	4	4.	4.	4	٥
	sequence	US-08-746-682A-14	US-08-597-236-14	US-09-134-000C-3685	PCT-US95-02251-18	US-09-592-685-2	US-08-479-722B-2	US-08-868-373-12	US-09-058-947A-4	US-09-489-039A-8648	US-09-549-441-37	US-09-919-039-40	US-08-727-034-7	US-08-727-034-3	US-09-949-016-8313	US-09-328-352-6682	US-09-359-268A-21		US-09-270-767-59862

ALIGNMENTS

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APPLICANT: Capplinaki, Kevin
APPLICANT: Capplinaki, Kevin
APPLICANT: Cimplinaki, Jonathan D.
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
CURRENT PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1998-07-22
PRIOR APPLICATION UNMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
SOFTWARE: PATENTING DATE: 1998-07-22
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 23
TYPE: PRI
TODDANICM: Sancharomyces Cerevisiae
                                                                                                                                                                                                                                                                                       US-09-359-268A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa = US-09-359-268A-8
                                                            APPLICANT: Peltz, Stuart
APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Nevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: THE FIDELI
TITLE OF INVENTION: THEREOP
FILE REFERENCE: 601-1-85N
                                                                                                                                                                                                                  Sequence 29, Application Patent No. 6630294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22 PRIOR APPLICATION NUMBER: 60/093,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                               VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                          A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS THE FIDELITY OF TRANSLATION TERMINATION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.2%;
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RESULT 4
US-09-270-984A-22
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SEQ ID NO 29
LENGTH: 380
TYPE: PRT
ORGANISM: Baccharomyces cerevisiae
            Sequence 22, Application US/09270984A Patent No. 6048965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                              Matches
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                             TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/016,4
PILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/724,354D FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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STREET:
TTY: La Jo.
CA
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                                                                                                                                                                          Match 92.2%;
Local Similarity 82.6%;
                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 VEVASVDAFQGREKDYIILSCVR 356
                                                                                                                                                              19;
                                                                                                                     1 VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VEVXTVDXFQGREKDXIILSCVR 23
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                                                                                                                                                                                                                                                   amino acid
GY: linear
                                                                                                    VEVASVDAFQGREKDYIILSCVR 779
                                                                                                                                                                                                                                                                                971 amino acids
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/016,482
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; Pred. No. 5.2e
1; Mismatches
                                                                                                                                                            1; Mismatches
                                                                                                                                                                           Score 95; DB 2;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                        07265/090001
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                                                                                                                                                            Gaps
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RESULT 5
US-09-177-431-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Dietz,
                                OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOSTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREST: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lise A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MAMMALIAN REGULATOR OF TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TYPE: Inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     STREET: 225 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                   FILING DATE:
                                                                                                                                                               COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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VENTION: MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                  IBM Compatible
SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.2%;
                                                                                                                                                                                                                                                                                                               HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95; DB 3;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 971;
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RESULT 6
US-08-724-354D-4
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                                                                       US-08-724-354D-4
                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FREESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Query Match
Best Local Similarity 78.:
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08724354D Patent No. 5994119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.3
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                           TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMAL
TITLE OF INVENTION: NONSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-9806
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDA
STREET:
STREET:
CJ
                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Passe, J. Peter
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                           TOPOLOGY:
                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                         1043 amino acids
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                     91.3%;
78.3%;
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Pred. No. 1.6e-09;
1; Mismatches 3
   Score 94; DB 2; Length 1043; Pred. No. 2.7e-09; 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                    Sequence 2, Application US/08724354D Patent No. 5994119
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.:
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6048965
                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Dietz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,984A
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LENGTH: 1043 amino aci
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NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 072
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APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskette
                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                      TITLE OF INVENTION:
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STREET: 4221
CITY: La Jolla
CTATE: CA
TICA
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                                                                                                                     NUMBER OF SEQUENCES:
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CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
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                                                                STREET:
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ZIP: 92037
                                                                ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
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STREET: 4225 Excutive Square, Suite 1400
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                                                                                                                             Dietz, Harry C.
VENTION: MAMMALIAN REGULATOR OF
VENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1043 amino acids
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Dietz, Harry C.

PENTION: MAMMALIAN REGULATOR OF DUAL
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78.3%;
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Pred. No. 2.7e-09;
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RESULT 9
US-09-270-984A-2
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INFORMATION FOR SEQ ID NO: 2:
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                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMAI
TITLE OF INVENTION: NONSEN
               SEQUENCE CHARACTERISTICS:
LENGTH: 1118 amino aci
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MEDIUM TYPE: Diskett
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SOPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CITY: La Jolla
STATE: CA
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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GY: linear
amino acid
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4225 Excutive Square,
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               1118 amino acids
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                                                              619-678-5099
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SYSTEM: Windows95
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78.3%;
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Pred. No. 2.9e-09;
2; Mismatches 3
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Suite 1400
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; ORGANISM: Human
US-09-949-016-10116
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US-09-949-016-10116
                                                          US-09-359-268A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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LENGTH: 1140
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Best Local Similarity 78.3%;
                                                                                                                                   SOFTWARE: I
SEQ ID NO 28
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Best Local Similarity
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                    Query Match
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/09359268A
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR ETLING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                        APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                              LENGTH: 41
TYPE: PRT
                                                                            ORGANISM: saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                         PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                     Czaplinski, Kevin
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83.5%;
73.9%;
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Pred. No. 3e-09;
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Pred. No. 2.9e-09;
Score 86; DB 4; 1
Pred. No. 3.1e-08;
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Best Local Similarity

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                                                                                                                                   US-09-902-540-16148
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16148
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16148,
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YKL017C
-09-538-092-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 483, App
Patent No. 67533
                                                                                                                                                                                                                                                                APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15949)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOPTWARE: CuraPatSegFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/178,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Saccharomyces
                                                                                                                                                   DRGANISM: Myxococcus xanthus
                                                                                                                                                                                     LENGTH: 211
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17; Conserva
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                                                                                   Similarity
                                 VEVXTVDXFQGREKDXIILSCVR 23
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73.9%;
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73.9%;
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Pred. No. 5.7e-08;
2; Mismatches 4
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                                                                Score 82; DB 4;
Pred. No. 8.3e-08;
1; Mismatches
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FILE DE INVESTE SON IN NUMBER: US/09/248,796A CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13 PRIOR PELICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 15170 LENGTH: 426 TYPE: PRT
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Search completed: April 18, 2005, 08:18:36
Job time : 28.708 secs
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                                                                                                                                                                                                                                     ; ORGANISM: Candida albicans
US-09-248-796A-15170
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US-09-248-796A-15170
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US-09-248-796A-19347
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US-09-248-796A-19347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19347
LENGTH: 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6747137
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19347, Appl. Patent No. 6747137 GENERAL INFORMATION:
                                                                                                                                                        Matches
                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN. TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
FUNRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/60/074,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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65.2%;
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Pred. No. 7.2e-07;
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Pred. No.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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.: /cgn2_6/ptodata/1/pubpaa/US07
.: /cgn2_6/ptodata/1/pubpaa/PCT_1
.: /cgn2_6/ptodata/1/pubpaa/US06
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/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
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2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

12 13	10	087	ப்பை	ں م	27	Result No.
86 86	889	9 9 9	94	95	97 95	Score
83.5 83.5	86.4	91.3	91.3	92.2 91.3	94.2	Query Match
562 677	1118 414	935	638	925 437	23 380	
15 16	16	16	16	15	16	BB
US-10-104-047-2003 US-10-476-924-9	US-10-474-553-6 US-10-652-334-28	US-10-424-599-205643 US-10-408-765A-1706 US-10-368-483-13780	US-10-425-114-57765 US-10-437-963-181690	US-10-369-493-2087 US-10-425-114-42857	US-10-652-334-8 US-10-652-334-29	ID
	Sequence 6, Appli Sequence 28, Appl	Sequence 205643, Sequence 1706, Ap	Sequence 181690,	Sequence 2087, Ap Sequence 42857, A	Sequence 8, Appli Sequence 29, Appl	Description

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70.9	71.8	71.8	72.8	٠	•	•	•	•	75.7	•	•	•	•	•	•	76.7			76.7	76.7	77.7	77.7	77.7	77.7		9.	٩	٩	80.6	.0	83.5
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111794,	22554, A	21435, A	1830, Ap	26, Appl	183044,	2884, Ap	×	21357, A	,88	216889,	185291,	1268, Ap	80, Appl	20334, A	37557, A	166322,	37833, A	241211,	38637, A	•	•	41078, A	•	•	•	•	37717, A	233501,	22, Appl	•	22

ALIGNMENTS

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US-10-652-334-8
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SEQ ID NO 8

LENGTH: 23

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae
PEATURE:
                                                                        Matches
                                                                                          Query Match
Best Local (
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Publication No. US20040115787A1
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Peltz, Stuart
APPLICANT: Caplinski, Kevin
APPLICANT: Ciman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION
TITLE OF INVENTION: THERROF
FILE REFERENCE: 601-1-85N
                                                                                                                                                                 OTHER INFORMATION: Xaa = any amino acid
                                                                                        Similarity
                                   VEVXTVDXFQGREKDXIILSCVR 23
                                                                                        94.2%;
                                                                                        Score 97; DB 16; 
; Pred. No. 3.6e-10;
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                                                                        Mismatches
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                                                                                                          Length 23;
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WE-10-425-114-42857
US-10-425-114-42857; Sequence 42857, Application US/10425114; Publication No. US20040034888A1
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; TYPE: PRT
; ORGANIZM: Schizosaccharomyces pombe
US-10-369-493-2087
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US-10-652-334-29
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US-10-652-334-29
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-29
PRIOR APPLICANTON NUMBER: US 60/360,039
PRIOR PREFICATION NUMBER: US 60/360,039
PRIOR PREFICATION NUMBER: US 60/360,039
PRIOR PREFICATION NUMBER: US 60/360,039
PRIOR PRIOR DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2087
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Best Local Similarity 82.6%;
Matches 19; Conservative
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Publication No. US20040115787A1
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Publication No. US20030233675A1
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CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
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APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 601-1-85N
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TYPE: PRT
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Local Similarity 82.6%;
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49 VEVASVDAFQGREXDFIILSCVR 771
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Pred. No. 2e-08;
1; Mismatches
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RESULT 6 US-10-437-963-181690

Sequence 181690, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

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APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT EILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42857
LENGTH: 437
TYPE: no-
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                                                                                                                                           ; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY058E07_FLI.pep US-10-425-114-57765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700476463_FLI.pep
US-10-425-114-42857
                                                                                                                                                                                                                 FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57765
LENGTH: 449
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
APPLICANT: Cao, Yongwei
                                                                         Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57765, Application US/10425114 Publication No. US20040034888A1
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                              ORGANISM: Glycine max
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19 IEVASVDSFQGREKDYIILSCVR 41
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                      1 VEVXTVDXFQGREKDXIILSCVR 23
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Kovalic, David K.
Kovalic, David K.
Screen, Steven E
Screen, Jack B
Vongwei
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                                                                     Conservative
                                                                                        91.3%;
78.3%;
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                                                                                      Score 94; DB 15;
Pred. No. 3.7e-08;
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Pred. No. 3.5e-08;
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                                                                                                       Length 449
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RESULT 8
US-10-408-765A-1706
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US-10-424-599-205643
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205643
LENGTH: 734
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                Sequence 1706, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 205643, Application US/10424599 Publication No. US20040031072A1
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: UNSURE NAME/KEY: UNSURE LOCATION: (1)..(638)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (1)..(734)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Soumitra S
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78.3%;
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78.3%;
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Pred. No. 6.4e-08;
2; Mismatches 3
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Pred. No. 5.4e-08;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12790
LENGTH: 992
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US-10-474-553-6 ·
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US-10-408-765A-1706
Sequence 6, Application US/10474553

Publication No. US20040161765A1

GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING DISEASE
TITLE OF INVENTION: GENES USING NONSENSE-MEDIATED DECAY INHIBITION
FILE REFERENCE: JHV-020.25
CURRENT APPLICATION NUMBER: US/10/474,553
CURRENT FILING DATE: 2003-10-10
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1706
LENGTH: 935
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Best Local Similarity
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APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 91.3%;
l Similarity 78.3%;
l8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                     VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                        IEVASVDAFQGREKDFIILSCVR 711
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Taylor, Steven W.
Glenn, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                           91.3%;
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Pred. No. 9e-08;
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Pred. No. 8.4e-08;
2; Mismatches 3
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PRIOR APPLICATION NUMBER: 60/283,920

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US-10-104-047-2003
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US-10-652-334-28
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US-10-474-553-6
                                                                                                                                                                                                                                                              Sequence 2003, Application US/10104047 Publication No. US20030236392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                     SEQ ID NO 2003
LENGTH: 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Publication No. US20040115787A1
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                                                                                                           APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR PILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dinman, Jonathan D. TITLE OP INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 601-1-85N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/652,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Peltz, Stuart APPLICANT: Czaplinski, 1 APPLICANT: Dinman, Jona
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NUMBER OF SEQ ID NOS: 10
                                                                                             SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-08-28
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10-104-047-2003
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TYPE: PRT
               ORGANISM: Homo sapiens
                                     TYPE: PRT
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Pred. No. 9e-0
2; Mismatches
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US-10-369-493-22264

Sequence 22264, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PF-0960 USN
CURRENT APPLICATION NUMBER: US/10/476,924
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/USO2/14276
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US 60/288,598
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/291,776
PRIOR APPLICATION NUMBER: US 60/291,776
PRIOR APPLICATION NUMBER: US 60/292,172
PRIOR APPLICATION NUMBER: US 60/292,172
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 46
SOFTWARE: PERL Program
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10476924 Publication No. US20040152093A1
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Best Local
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                                                                                                            Query Match
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2948827CD1
                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                            LENGTH:
                                                                     Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| ||| || ||: ||||||| 446 VQVSTVDAFQGAEKEIIILSCVR 468
561 VQVSTVDAFQGAEKBIILSCVR 583
                                                                                                                                                                                                                                                                677
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                                    1 VEVXTVDXFQGREKDXIILSCVR 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAUGHN, Mariah R.; LAL, Preeti G.;
YUE, Hulbin; HAFALIA, April J.A.;
LEE, Ernestine A.; ISON, Craig H.;
BECHA, Shanya D.; GURURAJAN, Rajagopal;
EMERLING, Brooke M.; GRIFFIN, Jennifer J.
TANG, Y. Tom; LU, Dyung Aina M.;
YAO, Monique G.; CHANLA, Narinder K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAMKUMAR, Jayalaxmi; GANDHI, Ameena R.;
LEE, Soo Yeun; RICHARDSON, Thomas W.;
YANG, Junning; BILLIOTT, Vicki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HE, Ann; AZIMZAI, Yalda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAUMANN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yan; THANGAVELU, Kavitha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brigette E.; SWARNAKAR, Anita; Neil
                                                                                           83.5%;
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                                                                         2;
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Pred. No. 1.3e-06;
                                                                                           Score 86; DB 16;
Pred. No. 1.6e-06;
                                                                         Mismatches
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Sequence 96, Application US/10144194A

| Publication No. US20030215809A1
| GENERAL INFORMATION:
| APPLICANT: OriGene Technologies Inc
| TITLE OF INVENTION: Regulated Breast Cancer Genes
| FILE REFERENCE: 3U 103 R1
| CURRENT APPLICATION NUMBER: US/10/144,194A
| CURRENT FILING DATE: 2002-06-12
| NUMBER OF SEQ ID NOS: 114
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 96
| LENGTH: 828
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-144-194A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22264
LENGTH: 683
LENGTH: 683
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22264
Search completed: April 18, 2005, 09:04:07 Job time: 81.5912 secs
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US-10-144-194A-96
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                                                                                                                                                                                Query Match 80.6%; Score 83; DB 15; Length 828; Best Local Similarity 68.2%; Pred. No. 6.9e-06; Matches 15; Conservative 4; Mismatches 3; Indels
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Best Local Similarity 73.5
Matches 17; Conservative
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CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                         2 EVXTYDXFQGREKDXIILSCVR 23
|| || || || || :| :| :| ||
521 EVDTYDAFQGRQKDCVIVTCVR 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                         DB seq
                                                                                                                                                                                                                                        Score
 length: 0
length: 2000000000
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                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                            PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Maximum Match 100%
Listing first 45 summaries
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               VEVXTVDXFQGREKDXIILSCVR
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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$53416
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A47500
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                      Dna2p - fission ye hypothetical helic hypothetical prote
                                             SEN1 protein - yea
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        related to SEN1 pr
insulin II gene en
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protei
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ALIGNMENTS

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prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9593.05c; protein YMR080c; UPF1 protein
C;Species: Saccharomyces cerevisiae
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S23408; A44388; S54455
R;Altamura, N.; Groudinsky, O.; Dujardin, G.; Slonimski, P.P.
J. Mol. Biol. 224, 575-587, 1992
A;Mol. Biol. 224, 575-587, 1992
A;Reference number: S23408; MUID:92235815; PMID:1314899
A;Accession: S23408; MUID:92235815; PMID:1314899
A;Accession: S23408; MUID:92235815; PMID:1314899
A;Accession: S23408
A;Residues: 1-971 <ALT>
A;Coss = references: UNIPROT:P30771; EMBL:X62394; NID:g4022; PIDN:CAA44266.1; PID:g4023
R;Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S62476
hypothetical protein SPAC16C9.06c - fission yeast (Schizosaccharomyces pombe) c;Species: Schizosaccharomyces pombe C;Species: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S62476; T37779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q09820; EMBL:Z54366; NID:g1019812; PIDN:CAA91194.1; PID:g132 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995 A;Reference number: Z21745 A;Reference number: Z21745 A;Recession: T37779
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A;Residues: 11-935 <BA2>
A;Cross-references: EMBL:Z54366; PIDN:CAA91194.2; GSPDB:GN00066; SPDB:SPAC16C9.06c
A;Experimental source: strain 972h-; cosmid c16C9
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A;Molecule type: DNA
A;Residues: 1-935 <BAD>
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Local Similarity 82.6%;
hes 19; Conservative
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Pred. No. 1.2e-08;
1; Mismatches 3;
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C;Accession: T46441
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23032
A;Accession: T46441
A;Accession: T46441
A;MOLECULE (1-239 <AAA>
A;Residues: 1-239 <AAA>
A;Residues: UNIPROT:Q9NSW3; EMBL:AL137700
A;Cross-references: UNIPROT:Q9NSW3; EMBL:AL137700
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R;Page, M.F.; Carr, B.; Anders, K.R.; Grimson, A.; Anderson, Mol. Cell. Biol. 19, 5943-5951, 1999
                                                                      A; Molecule type: mRNA
A; Residues: 1-239 < AA
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A;Residues: I-1069 <PAG>
A;Cross-references: UNIPROT:076512; EMBL:AF074017; NID:g3328176; PIDN:AAC26789.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1069 < P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonsense-mediated mRNA decay trans-acting factor - Caenorhabditis elegans C_iSpecies: Caenorhabditis elegans
                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                      hypothetical protein DKFZp434C0927.1 - C; Species: Homo sapiens (man)
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A;Reference number: Z22389; MUID:99384262; PMID:10454541
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A;Map position: 13R
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A; Residues: 1-971 <GEN>
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A; Accession: S54455
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A;Experimental source: strain AB972
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                                                                                                                                                                                                                                                          Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
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69.6%;
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Pred. No. 2.4e-07
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Pred. No. 1.2e-08
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tRNA-splicing endonuclease positive effector - fission yeast (Schizosacchar C;Species: Schizosaccharomyces pombe C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T40065 C;Accession: T40065 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F. submitted to the EMBL Data Library, December 1998
                                                                                                                                                                                                                                                                      RESULT 6
T40065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable purine nucleotide-binding protein YKL017c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: S34700; S37830; S37834 R;Mieman, S.; Voss, H.; Schwagaer, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Groth submitted to the EMBL Data Library, July 1993 A;Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome A;Reference number: S34879
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S34700
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C;Superfamily: probable DNA helicase MJ0104
C;Keywords: ATP: P-loop; purine nucleotide l
F;229-236/Region: nucleotide-binding motif l
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A;Residues: 1-683 <RIE>
A;Cross-references: EMBL:Z28017; NID:g486006; PID:g486007; MIPS:YKL017c
A;Experimental source: strain S288C
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A;Residues: 1-683 <WI2>
A;Cross-references: EMBL:Z28017; NID:g486006; PID:g486007; MIPS:YKL017c
A;Experimental source: strain S288C
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A;Reference number: S37825
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                                         A;Status: preliminary; translated
                                                                  A; Reference number: Z21903
A; Accession: T40065
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A;Accession: $37834
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A; Residues: 1-683 <WIE>
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                  ;Molecule type:
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1-1944 <LYN>
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73.9%;
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Pred. No. 3.5e-0
                                                from GB/EMBL/DDBJ
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Pred. No. 1
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1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e-07;
                                                                                                                                                                                                                                               fission yeast (Schizosaccharomyces
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C;Geneti
A;Gene:
A;Map po
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                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-530 < AQF>
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                                                                                                                                                                                                                                                                                     Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                   R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                    DNA helicase -
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A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription control factor enhancer-binding protein - Methanobacterium thermoautotroph
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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A;Experimental source: strain 972h-; cosmid c29A10
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                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                     ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
;Accession: D70476
                                                                                                                                                        Cross-references: UNIPROT:067840; Experimental source: strain VF5
                                                                                                                                                                                                                    Status: preliminary; nucleic acid sequence not shown;
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17; Conser
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17; Conserv
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Similarity 65.2%;
15; Conservative
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VEVKTVDGFQGREKEVIIISFVR
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                     VEVXTVDXFQGREKDXIILSCVR
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                                                                                                                                                                                                                                                                                                                                                                                  Aquitex aeolicus
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                                                           77.7%;
larity 73.9%;
Conservative
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larity 73.9%;
Conservative
                                                           Score 80; DB
Pred. No. 3.3e
2; Mismatches
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Pred. No.
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Pred. No. 2.6e-06;
2; Mismatches 4
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                                                                                                                                                                      GB:AE000770; NID:g2984274;
472
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                                                                          DB 2; 1
3.3e-06;
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5.1e-06;
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J.; Gibson, R.; Jiwani,
ing, J.; Reeve, J.N.
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A;Gene: T20K24.14; At2g19120
A;Map position: 2
A;Introns: 250/1; 310/1; 342/1; 383/2; 427/3; 1016/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon, L.euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A;Cross-references: UNIPROT:O64476; EMBL:AC002392; NID:g3176701; PID:g3176714
A;Experimental source: cultivar Columbia
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A; Residues: 1-1090 <STO>
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A; Accession: G84572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_iTitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A_iReference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z14167
A; Accession: T00533
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R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.(
submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
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A; Accession: B75105
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C;Superfamily: probable DNA helicase MJ0104
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C;Accession: B75105
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C;Species: Ругососсия арукая
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60.9%;
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                                                                                                                Score 80; DB 2;
Pred. No. 6.6e-06;
5; Mismatches 4
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Pred. No. 4e-06;
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967 IYINTVDAFQGQERDVIIMSCVR 989

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RESULT 13
E71080
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Benito, M.S.; Umayam, L.; Tallon, J.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84446
                                                                                                                                                                                                                                                                                                                  A; Map position: 2
C; Superfamily: probable DNA helicase MJ0104
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submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02699; D84446 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable helicase At2g03270 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T18E12.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Residues: 1-1311 <BEV>
A;Residues: 1-1311 <BEV>
A;Cross-references: UNIPROT:Q9SZW3; EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.130
A;Experimental source: cultivar Columbia; BAC clone F6G3
probable DNA-binding protein -
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A; Accession: T08986
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                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002093; NID:g4335770; PIDN:AAD17447.1; GSPDB:GN00139
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Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                 Query Match
Best Local
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es 15; Conserv
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60.9%;
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65.2%;
Pyrococcus horikoshii
                                                                                                                                                                                                                     ; Score 79; DB
; Pred. No. 5.9e
4; Mismatches
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Pred. No.
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  A;Cross-references: UNIPROT:Q9AVZ7; GB:AJ010592; NID:g12580756;
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M.; Ohfuku, Y.; Funahasnı, 1.; 1918
DNA Res. 5, 55-76, 1998
A,Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A,Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                        Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1999 #^^~~
                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-648 <KLE>
A;Cross-references: UNIPROT:OZ8883; GB:AB001009; GB:AB000782; NID:g2689332; PIDN:AAB8986(
C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                  A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Moese, C.R.; Venter, J.C. A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not A;Molecule type: DNA A;Residues: 1-656 <KAW>
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                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_rev
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                                                                                                      Query Match
Best Local
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4.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                  Matches
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556 VEVSSVDGFQGREKEVIIISFVR 576
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                                                                                                      Similarity
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Pred. No.
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Pred. No. 1.4e-05;
3; Mismatches '
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                                                                                                                                                                                                                                                                                                                  sulfate-reducing
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J.; Kushida,
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irkness, E.F.,
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hypothetical protein component of a tRNA splicing complex [imported] - Guillardia theta C;Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: E91113
                                                                                            R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: E90113
A; Molecule type: DNA
A; Residues: 1-692 < DOU>
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1: uniprot_sprot:*
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                   Q6SYT5
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westbof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome D complete sequence.
ORFNames=CAGL0D043129;
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ATP-binding; Helicase; Hydrolase; Hypothetical Nonsense-mediated mRNA decay; Z17c-finger.

ZN_FING 52 80 C2H2-type (atypica ZN_FING 104 134 C4-type (Potential NP_BIND 414 421 ATP (By similarity
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InterPro; IPRO06935; ResIII.
Pfam; PF04851; ResIII; 1.
SMART; SM00487; DEXDC; 1.
SEQUENCE 964 AA; 108274 M
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InterPro; IPR003593; AAA_ATPase.
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ATP (By similarity).
MW; 4A5D63C82826E864 CRC64;
                                                                                                                                        ; Score 95; DB
; Pred. No. 1.4e
1; Mismatches
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Pred. No. 1.3e-08;
1; Mismatches 3
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RESULT 4
NAM7_YEAS
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InterPro; IPR00594; RNA_rec_mot.

Iffen; PF04851; ResIII1, RESIII1, PF04851; PS00030; RRM RNP 1; UNKNOWN 1.

PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.

PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.

PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
                                                                                                                                                                                                 7 YEAST
NAM7 YEAST
P30771;
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Dafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Bairame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Micaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Michael C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
NAM7 protein ((Nuclear accomodation of mitochondria 7 protein)
Nonsense-mediated mRNA decay protein 1) (Up-frameshift suppressor
Name=NAM7; Synonyms=IFS2, MOP4, UPF1; OrderedLocusNames=YMR080C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces. NCBI_TaxID=284590;
                               Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes,
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                               Name=NAM7; Synonyms=IFS2,
ORFNames=YM9582.05C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382122; CAH02214.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bouchier C., Cauu.
Bouchier P., Souciet J.L.;
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25-OCT-2004 (TrEMBLrel. 28, Last
25-OCT-2004 (TrEMBLrel. 28, Last
25-OCT-2004 (TrEMBLrel. 28, Last
Kluyveromyces lactis strain NRRL
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        Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NRRL
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                                                              Saccharomyces cerevisiae (Baker's yeast).
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STRAIN=NRRL Y-1140;
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                                                                                                                                                                                                                                                                                                        VEVASVDAFQGREKDYIILSCVR 777
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                                                                                                                                                                                                                                                                                                                                                                                         92.2%;
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Pred. No.
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N.A.

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SMART; SM00382; AAA; 1.

DR SMART; SM00382; AAA; 1.

DR SMART; SM00487; DEXDC; 1.

KW ATP-binding; Helicase; Hydrolase; Mitochondrion; W Nonsense-mediated mRNA decay; Nuclear protein; T ZN FING 70 98 C2H2-FING 122 152

T NP_BIND 422 152
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                                                                            Query Match
Best Local
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EMBL; M76659; AAA35197.1; -.
EMBL; Z49259; CAA89226.1; -.
PIR; S23408; S23408.
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"Mof4-1 is an allele of the UPP1/IPS2 gene which affects both mRNA
"mof4-1 is an allele of the UPP1/IPS2 gene which affects both mRNA
turnover and -1 ribosomal frameshifting efficiency.";
EMBO J. 15:5726-5736(1996).

-I- PUNCTION: Probable helicase involved in mitochondrial functions.
Required for rapid turnover of mRNAs containing a premature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altamura N., Groudinsky O., Dujardin G., Slonimski P.P.;
"NAM7 nuclear gene encodes a novel member of a family of helicases
with a Zn-ligand motif and is involved in mitochondrial functions in
                                                                                                                                                                                                                                                               SGD; S000004685; NAM7.
GO; GO:0005737; C:cyroplasm;
InterPro; IPR003593; AAA ATPR
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene products that promote mRNA turnover in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  or send
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MEDLINE=97051830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92236591; PubMed=1569946; Leeds P.F., Wood J.M., Lee B.S.,
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STRAIN=R23/50
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92235815; PubMed=1314899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translational termination codon.
SUBCELLULAR LOCATION: Present predominantly in the cytoplasm, is also found in small quantities in the nucleus.
SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
 VEVASVDAFQGREKDYIILSCVR 779
                             VEVXTVDXFQGREKDXIILSCVR
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                                                                                                                               971 AA;
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                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae.";
224:575-587(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8896465;
                                                                             92.2%;
82.6%;
                                                                                                                               MW; 9161AFB0BE6747FE CRC64
                                                               Score 95; DB
Pred. No. 1.46
1; Mismatches
                                                                                                                                             , Nuclear protein; Zinc-finger.
C2H2-type (atypical) (Potential).
C4-type (Potential).
ATP (By similarity).
                               23
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 2:
01-OCT-2002 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Rentl protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2004) to the EMBL/GenBank/DDBJ EMBL; AE016815; AAS50792.2; -. GO; GO:0000166; P:nucleotide binding; IEA. InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Rent1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRALN-STCC 10895;
Voegeli S.E., Dietrich F.S.,
Philippsen P.;
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             Jones S.J., Marra M.A.; "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                               TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Pred. No. 1
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Sciurognathi; Muridae; Murinae; Mus
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Pellenz S., Tekaia F., Wesolowski-Louvel M., Westhof E., With B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.,
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Best Local S
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Q6BPM3;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
EMBL; CR382137; CAG88086.1; -.
InterPro; IPR011545; DEAD/DEAH_N.
SMART; SM00487; DEXDC; 1.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030916; AAH30916.1; -.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=DEHA0B13002g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genolevures;
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                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                       110705 MW; 14DBD331A4E37E0D CRC64;
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78.3%;
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                                                                                                Score 94; DB 2;
Pred. No. 2.2e-08;
2; Mismatches 3
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Pred. No.
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of strain CBS767
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Best Local
                                                                                                                                                                   PubMedal4998527; DOI=10.1016/j.fgb.2003.12.003;
Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M. Posker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S., O'Neil S., Pertea M., Price C., Rabbinowitsch E., Rajandream M-A., Salzberg S., Saunders D., Seegar K., Sharp S., Warren T., Salzberg S., Saunders D., Seegar K., Sharp S., Warren T., Denning D.W., Barrell B., Hall N.;
"Insight into the genome of Aspergillus fumigatus: analysis of a 922 kb region encompassing the nitrate assimilation gene cluster.";
Fungal Genet. Biol. 41:443-453(2004).

EMBL, BX649606; CAF32021.1; -
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01-JUN-2002 (TrEMBLrel. 25, Last sequence update)
01-GT-2003 (TrEMBLrel. 25, Last annotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible regulator of nonsense transcripts.
Name-AEA5C11.22c;
Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulator of nonsense transcripts, ORFNames=AfA5cll.22c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
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05-JUL-2004 (TrEMBLrel. 27, Last ann
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InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR006935; ResIII.
Pfam; PF04851; ResIII; 1.
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GO; GO:0000166; F:nucleotide binding; I
GO; GO:0015668; F:type III site-specifi
GO; GO:0009307; P:DNA restriction; IEA.
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Denning D.W., Anderson M.J., Barrell B.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
                                                          InterPro; IPR011545; DEAD/DE
InterPro; IPR006935; ResIII.
Pfam; PF04851; ResIII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
PubMed=14998527; D
                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
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SM00487; DEXDc; 1.
                               SM00487;
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   1079 AA;
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                                   DEXDc;
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78.3%;
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MW.
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Last annotation updat
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Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding; IEA
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A8907E6FA8500E63 CRC64;
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A Galagan J.E. Calvo S.E. Borkovich K.A. Selker B.U., Rehman B.,
A Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
A Rikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
A Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun B.L.,
A Celter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
A Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
A Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
A Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S.,
A Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
A Rasmussen C., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A DeSouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
A Paulsen O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
A Paulsen I., Sachs M.S., Lander B.S., Nusbaum C., Birren B.,
I Mature 422:899-868 (2001).
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16-OCT-2001 (Rel. 40, Created)
InterPro; IPR006935; ReBIII.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
                                                    EMMBL, AL451022; CAC18314 1; -.
EMMBL, AABXO1000272; EAA31997.1; -.
InterPro; IPR003593; AAA ATPASE.
InterPro; IPR001410; DEAD.
                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way most field and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12712197; DOI=10.1038/nature01554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=74-OR23-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=74-OR23-1A / PGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulator of nonsense transcripts 1 homolog ORFNames=2E4.130, NCU04242.1;
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                                                                                                                                                      or send an
                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "What's in the genome of a filamentous fungus? Analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Eliminates the production of nonsense-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEVASVDAFQGREKDFILLSCVR 798
                                                                                                                                                        email to license@isb-sib.ch).
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78.3%;
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Pred. No.
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Kempken F., Maier J.,
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Neurospora.
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                                                                                                                                                                                                                                                    and the EMBL outstation
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RESULT 12
Q6GNR2
ID Q6GNR
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Q6GNR2 Q6GNR2;

PRELIMINARY;

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RESULT 11
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Best Local S
Matches 18
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Best Local S
Matches 18
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ZN_FING 1
ZN_FING 1
NP_BIND 4
DOMAIN
                                                                                                                                                                                                                                                                                                                         "Comparative analysis of human 19p12-13 region in Fugu and mouse."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Eliminates the production of nonsense-containing (By similarity).
                                                                                              ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNT1_FUC
Q98TR3;
                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              Pugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoptergogii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                EMBL; AJ301641; CAC33025.1; -.
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced throu between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
05-JUL-2004 (Rel. 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUGRU
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                                                                                                                                              Zinc-finger.
                                                                                                                                                          ATP-binding;
                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=RENT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                      TaxID=31033;
801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUGRU
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                                                18;
                                                          Similarity
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                VEVXTVDXFQGREKOXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVXTVDXFQGREXDXIILSCVR
VEIASVDAFQGREKDFIILSCVR
                                                                                                                                                                     IPR006935;
                                                                                              113
165
474
1097
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163
477
59
                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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78.3%;
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78.3%;
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Last annotation update)
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                                                                                                                                                           Hydrolase; Nonsense-mediated mRNA decay;
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                                                                                             C2H2-type (atypical) (C4-type (Potential).
ATP (Potential).
B MW; FDCC7C2B4B26AC54 (
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                                               <u>ب</u>
                                                             Score 94; I
Pred. No. 2.
                                                           Pred.
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Pred. No. 2.
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C4-type (Potential).
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Poly-Asp.
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                                                                                                FDCC7C2B4B26AC54 CRC64;
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2.5e-08;
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RESULT 13
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scheetz T.E.,
Schapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stempstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Macdan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Macdan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Tuchman J.W., Green E.D., Dickson M.C.,
A Whiting M., Tuchman J.W., Green E.D., Dickson M.C.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S. J. Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                 Q7ZVZ4
Q7ZVZ4;
Q1_JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073441; AAH73441.1; -.
GO; GO:0015668; F:type III site-specific deoxyribonuclease ac.
GO; GO:0009307; P.DNA restriction; IEA.
ORFNames=zgc:55472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                             Regulator of nonsense transcripts 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006935; ResIII. Pfam; PF04851; ResIII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.;
"Generation and initial analysis and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12454917; DOI=10.1002/dvdy.10174; sberg R.L., Wagner L., Pontius J., Clifton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%;
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Last
                                                    Last sequence update)
Last annotation update)
                                                                                                              Created)
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2; Mismatches
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annotation update)
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RESULT 14
RNT1_RNT1L
ID RNT11
AC Q9EPI
DT 16-00
DT 16-00
DT REGUL
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GN Name-
GN SEQUI
RR (1)
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RA Alteschul S.F., Zeebberg B., Buetcow K.H., Schaefer C.P., Bhat N.K.,

RA Alteschul S.F., Zeebberg B., Buetcow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Schapteton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robest S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,

RA Jones S. T. Marra M A.
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NTTI_MOUSE

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REPUTO; Q99PR4;

T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2001 (Rel. 40, Last sequence update)
T 05-UUL-2004 (Rel. 44, Last annotation update)
Regulator of nonsense transcripts 1 (Nonsense (NORFI) (Up-frameshift suppressor 1 homolog).
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases EMBL, BC045353; AAH45353.1; -.
ZFIN; ZDB-GENE-040426-3836; zgc:55472.
GO; GO:0015668; F:type III site-specific deoxyribonucle; GO; GO:000307; P:DNA restriction; IEA.
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Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
and mouse cDNA sequences.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformo
Cyprinidae; Danio.
                                                  MEDLINE=21067878; PubMed=11152657; Medghalchi S.M., Frischmeyer P.A., Lawler A.M., Dietz H.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas
Strausberg R.L., Feingold E.A., Grouse L.H., Derge
                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                               STRAIN=129/Sv;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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Pfam; PF04851; ResIII; 1.
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                             "Rent1,
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18; Conserv
                             a trans-effector of nonsense-mediated
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nilarity 78.3%;
Conservative
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     embryonic
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                                                                                                                                                                                                                                                             ; Chordata;
; Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3215FEBDDC63E3CB CRC64;
                                                                                   DOI=10.1093/hmg/10.2.99;
Mendell J.T., Kelly A.G.,
                                                                                                                                                                                                                                                                                                                                                                           ( Nonsense
( homolog) .
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                                mRNA decay, is
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; Murinae; Mus
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SEQUENCE FROM N.A. Selg M., Strande J Jack H.-M.;

Strande J.,

chromosomal localization and expression of murine ing factor 1 (mNORF1), ";

Beck-Engeser G.B.J., Liehr T., Winkler T.,

Mol. Genet. 10:99-105(2001)

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                                                              Matches
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Patekran T.W.
                                                                                                                                                                                                                                                            DOMAIN
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                       NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic Branch reducing factor nonsense mRNA reducing factor nonsense with the reducing factor nonsense reducing factor 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF322655;
EMBL; BC052149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mammari, stability.";
stability.";
watl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97008109; PubMed-8855285; DOI-10.1073/pnas.93.20.10928; Perlick H.A., Medghalchi S.M., Spencer F.A., Kendzior R.J. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Sv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:107995; Rent:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian orthologues of a yeast regulator of nonsense transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Eliminates the production of nonsense-containing RNAs Essential for embryonic viability.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the DNA2/NAM7 hélicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF322655; AAG42830.1; -. BC052149; AAH52149.1; -. AF182947; AAK08652.1; -.
                                                              18;
  1 VEVXTVDXFQGREKDXIILSCVR 23
                                                                                                                                                                                                                                                                                                                                                                                                           IPR006935; ResIII.
                                                                                                                                                                         1026
126
178
487
60
                                                              Conservative
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1113
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208
494
                                                                                      91.3%;
78.3%;
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                                                                                                                                                                                                                                                                                    Hydrolase; Zinc-finger.
Ala/Gly/Pro-rich.
Gln/Ser-rich.
C2H2-type (atypical) (Potential).
                                                        ; Score 94; DB
; Pred. No. 2.5e
2; Mismatches
                                                                                                                                                                         ¥ >
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                                                                                                                                                                                                    C4-type (Potential).
ATP (Potential).
A -> P (in Ref. 2).
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                                                                                                                                                                            BFE8D50AD49DAA54 CRC64;
                                                                                         DB 1;
2.5e-08;
                                                              3; Indels
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                                                                                                                                                                                                                                                                                    SOURCE REPORT OF THE PROPERTY 
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                                                                                                                                      Matches
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                  Selg M., Strande J.L., Lichr T., Roth B., Beck-Engeser G
Winkler T.H., Jack H.M.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY597038; AAT46119.1; JOINED.
EMBL; AY597039; AAT46119.1; -
InterPro; IPR006935; ResIII.
Pfam; PF04851; ResIII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Rent1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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816
                                                                                                                                      18;
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                                            VEVXTVDXFQGREKDXIILSCVR 23
VEIASVDAFQGREKDFIILSCVR 838
                                                                                                                                                                                                                                                                                    1113 AA;
                                                                                                                                      Conservative
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                                                                                                                                                                       91.3%;
78.3%;
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27,
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Last annotation update)
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                                                                                                                                                                       Score 94; DB 2;
Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                                    689B4472FE93B576 CRC64;
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                                                                                                                                                                                                             Length 1113;
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Search completed: April Job time: 97.0292 secs 18, 2005, 08:15:48

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lotosul Amola Bood sint

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Database
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Listing first 45 summaries
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                                                                                                                                                                                                                                                          DB 80
                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
A Geneseq_16Dec04:*
1: geneseqp1990s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
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                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                   2105692
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Regult No.	Score	Query Match	Length	80	ID	Description
1	75	94.9	18	ωį	AAY77812	Aay77812 Motif IX
N	75	•	18	7	ABW01185	Saccha
ω	75	•	18	œ	ADP44111	Adp44111 Yeast tra
4	73	•	415	w	AAY77813	Aay77813 Yeast Mtt
υ	73	•	415	7	ABW01201	Saccha
σ	73	•	415	8	ADP44127	Adp44127 Yeast hel
7	73	92.4	992	8	ADS23757	Ads23757 Bacterial
8	73	•	1944	8	ADN19868	Adn19868 Bacterial
9	72	91.1	98	ű	ABP07670	Abp07670 Human ORF
10	71		471	w	AAY77815	Aay77815 Yeast Sen
11	71	•	472	7	ABW01202	Sacche
12	71	89.9	472	80	ADP44128	Adp44128 Yeast hel
13	71	•	2000	σ	ABR53451	Abr53451 Protein 8
14	71	89.9	2000	7	ADK64622	Adk64622 Disease t
15	71	•	2231	8	ADN19177	Adn19177 Bacterial
16	70	88.6	648	8	ADS41904	Ads41904 Bacterial
17	70	•	650	8	ADN20231	
18	70	•	653	8	ADS43215	Ads43215 Bacterial
19	70	88.6	654	4	AAB96566	Aab96566 Putative
20	70		655	4	AAB62031	Aab62031 Recombina
21	70		656	8	ADN18615	Adn18615 Bacterial
22	69	87.3	373	8	ADR10398	Adr10398 Human pro
23	69	•	688	8	ADN47941	Adn47941 Thermococ
24	69	87.3	797	N	AAW36508	Aaw36508 Human REN
25	69	87.3	925	8	ADN19434	Adn19434 Bacterial

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
62	62	63	64	65	65	67	67	67	67	68	68	68	68	68	68	69	69	69	69
78.5	78.5	79.7	81.0	82.3	82.3	84.8	84.8	84.8	84.8	86.1	86.1	86.1	86.1	86.1	86.1	87.3	87.3	87.3	87.3
712	698	818	693	986	171	663	648	642	611	971	971	971	380	380	380	1140	1118	1043	935
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ADS44332	ADM25464	ADK68058	ADN22619	AAO26745	AAB33009	ADS43005	ADS42927	ADS43096	ADS21255	ADK64706	ABR53412	AAY98057	ADP44131	ABW01205	AAY77814	AAY21377	ABG73900	AAW36509	ADJ69900
Ad844332	Adm25464	Adk68058	Adn22619	Aao26745	Aab33009	Ad843005	Ad642927	Ads43096	Ads21255	Adk64706	Abr53412	Aay98057	Adp44131	Abw01205	Aay77814	Aay21377	Abg73900	Aaw36509	Adjessoo
Bacterial	Hyperther	Female re	Bacterial	988-mer r	Pinue rad	Bacterial	Bacterial	Bacterial	Bacterial	Disease t	Protein s	Yeast Upi	Yeast hel	Saccharon	Yeast Upf	Human HUP	Human REN	Murine RE	Human nea

ALIGNMENTS

RESULT 1
AAY77812
ID AAY7 31-MAY-2000 AAY77812; Motif IX comprised in a gene modulating translation termination. AAY77812 standard; peptide; 18 (first entry) ₿

Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic.

Unidentified.

Misc-difference

Location/Qualifiers

22-JUL-1998; 03-FEB-2000. WO200005586-A2. 22-JUL-1999; 98US-00120435. 99WO-US016802. /note= "reisdues indicated Xaa are unspecified"

Peltz S, Czaplinski K, Dinman ð

(UYNE-) UNIV NEW JERSEY.

WPI; 2000-171458/15.

New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl transferase activity e.g. Duchene/Becker Muscular Dystrophy.

Claim 41; Page 80; 89pp; English.

The invention provides a new multiprotein complex which can modulate peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and carry out translation termination in eukaryotic cella, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to modulate peptidyl transferase activity during translation in a cell. It can be administered therapeutically combined with a carrier in

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination. Vectors comprising polynucleotides encoding the complex (or antisense sequences) can be constructed and introduced into cells to interfere with complex expression and so modulate the efficiency of translation termination of mRNA and/or degradation of aberrant transcripts in a cell. Agents binding to the complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation termination of mRNA at a nonsense codon and/or promote degradation of aberrant transcripts in cells. The method can be used to identify agents/compositions modulating binding to MTT1, useful to identify genes. Sequences AAY77804-812 represent motifs I-IX comprised in the genes of the property and the property modulation of the second control of the second control of the second can be used to identify genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transferase activity, especially diseases resulting from a nonsense or frameshift mutation e.g. beta-thalassemia, beta-globin, Ducheme/Becker Muscular Dystrophy etc. It can be used to identify disease conditions involving a defect in the complex, by transfecting cells with encoding nucleic acid and determining the proportion of defective complex before and after transfection. It is also useful to screen for drugs involved i peptidyl transferase activity during translation, inhibiting the interaction between MTI and eRF3 or involved in enhancing translation
Identifying an agent that increases nonsense suppression, for antivira therapy, by contacting modulator of translation termination (Mttl) in
                                                                WPI; 2003-810549/76
                                                                                                                                                                                        22-JUL-1998;
                                                                                                                                                                                                                               22-JUL-1999;
                                                                                                                                                                                                                                                                                                                 US6630294-B1
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulator of translation termination; MTT1; helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae motif IX peptide.
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                                                                                                                                                NEW JERSEY MEDICINE & DENTISTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nonsense mutation; yeast
                                                                                                                                                                                        98US-0093685P
                                                                                                                                                                                                                               99US-00359268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Xaa may be any amino acid"
                                                                                                                                                                                                                                                                                                                                                                             label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Unknown
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                          "Xaa may be
                                                                                                         Dinman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                          any amino acid'
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RESULT 3
ADP44IN
ID ADP4
XX ADP4
XX ADP4
XX ADP4
XX YON
DT 18-N
XX Gene
KW Fran
KW Ovan
KW Von
KW Von
KW Von
KW WELL
KW VON
KW V
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; translation termination; RNA helicase; MTT1; frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae motif peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae with a test agent, and detecting specific binding to Mttl.
                                                                                                                                                                                                                                                 (PELT/)
(CZAP/)
(DINM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004
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                                                                                                                                        WPI; 2004-449400/42
                                                                                                                                                                                           Peltz S,
                                                                                                                                                                                                                                                                                                                                                                22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2003; 2003US-00652334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast translation termination modulation protein motif IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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18; Conserv
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DINMAN J D.
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                                                                                                                                                                                           Czaplinski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                98US-0093685P
99US-00359268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Any amino acid"
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                                                                                                                                                                                              ζ,
                                                                                                                                                                                                 Dinman
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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Identifying a test composition or agent that modulates the efficiency translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent inhibits the MTT1.

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RRESULT 4
AAY/7913
ID AAY/7
XX AAY/7
XX AAY/7
XX AAY/7
XX Yeas
XX Yeas
XX Hell
XW Hell
XW Hell
XW Hell
XW Hell
XW Hell
XX Hell
                                                      activity e.g. Duchene/Becker
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Claim 41; SEQ ID NO 9; 41pp; English

transcripts, and provide modulators (inhibitors/stimulators) of speptidyl transferase activity during initiation, elongation, termination and mRNA degradation of translation. The agents, which may be antagonists or agonists, are useful in screening, diagnostic and therapeutic purposes, for diseases or conditions resulting from or cause premature translation, such as beta-thalassaemia, beta-globin, Duchenne/Becker Muscular Dystrophy, Haemophilia B, Von Willebrand Disease, Ostrophy, Haemophilia B, Von Willebrand Disease, Ostrophy, Haemophilia B, Von Willebrand Disease, Pamilial Tumour, Hirschsprung disease, Cystic fibrosis, Kidney Stones, Familial hypercholesterolaemia, Retinitis Figmentosa, or Neurofibromatosis, Retinoblastoma, ATM or Costmann Disease. The present sequence represents the amino acid sequence of the yeast translation termination modulation protein motif IX. the RNA helicase MTT1 with a composition or agent under conditions permitting binding between the MTT1 and the composition, detecting specific binding of the test composition or agent to the MTT1. Indetermining if the test composition or agent inhibits the MTT1. The composition and methods are useful for modulating the fidelity of translation termination or for identifying agents that: affect the functional activity of mRNAs by altering frameshift frequency, permit monitoring of a termination event, promote degradation of aberrant The invention modulates the relates to a method of identifying a test composition that efficiency of translation termination comprising contacting

X#X6666666666666666666666666666666688

Sequence 18 B

र् Matches Query Match Local 18; Conservative Similarity 94.9%; 0 Score 75; ; Pred. No. Mismatches DB 8; I 0 Length 18 Indels 0 Gaps 0

μ IGFLXDXRRINVALTRAK 18

밁

AAY77813 standard; peptide; 415 AA AAY77813;

31-MAY-2000 (first entry)

Yeast Mttl protein fragment

Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eRF3; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;

Saccharomyces cerevisiae

WO200005586-A2

03-FEB-2000

22-JUL-1999; 99WO-US016802

22-JUL-1998; 98US-00120435

(UYNE-) UNIV NEW JERSEY.

Peltz S, Czaplinski K, Dinman

New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl

Example 1; Fig 1; 89pp; English.

comparation be administered therapeutically combined with a carrier in a cell. It can be administered therapeutically combined with a carrier in a cell. It can be administered therapeutically combined with a carrier in a cell. It can be administered therapeutically diseases associated with peptidyl combined with a carrier in a cell. It can be used to identify disease conditions or composition of complex, by transferting from a nonsense or complex by transferting cells with encoding complex carrier in the complex, by transferting cells with encoding complex or interaction between MTTl and eRF3 or involved in enhancing translation complex comprising polynucleotides encoding the complex (or interaction between MTTl and eRF3 or involved in enhancing translation complex expression and so modulate the efficiency of complex expression and so modulate the efficiency of complex can be constructed and introduced into cells to complex expression and so modulate the efficiency of complex can be complex complex can be identified complex can cell. Agents binding to the complex can be identified complex at a nonsense codon and/or promote degradation of aberrant compositions modulate the efficiency of translation termination of compositions modulating binding to MTT1, useful to identify genes.

Compositions modulating binding to MTT1, useful to identify genes.

Compositions and/or promote degradation of aberrant compositions and/or promote degradation of aberrant compositions modulating binding to mTT1, useful to identify genes. peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of Translation Termination) and the conserved proteins known to interact and group I helicases carry out translation termination in eukaryotic cells, peptidyl eukaryotic release factor (eRF) 1 and eRF3. The complex can be used to provides a new multiprotein complex which can

Sequence 415 AA;

Matches Query Match Best Local Similarity 15; Conservative 92.4%; 1; Score 73; DB 3; Pred. No. 1.9e-05; 1; Mismatches 2 Length 415 Indels <u>.</u> Gaps 0

문 δ

398 ب

IGFLXDXRRINVALTRAK 18 IGFLRDKRRLNVÄLTRÅK 415

ABW01201 standard; protein; 415

ABW01201

15-JAN-2004 (first entry)

Saccharomyces cerevisiae modulator of translation termination protein

Modulator of translation termination; MTT1; helicase B; antiviral; therapy; HCSB; nonsense mutation; yeast.

Saccharomyces cerevisiae

US6630294-B1

07-OCT-2003.

22-JUL-1999; 99US-00359268

22-JUL-1998; 98US-0093685P

UNIV NEW JERSEY MEDICINE & DENTISTRY

Peltz S, Czaplinski K, Dinman JD;

WPI; 2003-810549/76

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RESULT 6
ADP44127
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Best Local
                                                                                  Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTTI with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                           Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinits Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast; enz;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; buchenne/Becker Muscular Dystrophy; Haemophilia A; Haemophilia B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae MTT1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an agent that increases nonsense suppression, for antiviral therapy, by contacting modulator of translation termination (Mttl) in Saccharomyces cerevisiae with a test agent, and detecting specific
                                                                       composition or agent, inhibits the MTT1.
                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; translation termination; RNA helicase; MTT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding to Mtt1.
                                            Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                    US2004115787-A1.
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                                                                                                                                               WPI; 2004-449400/42.
                                                                                                                                                                                                                                                                 22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                          28-AUG-2003; 2003US-00652334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast helicase Mttl.
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                                                                                                                                                                          Czaplinski K,
                                         SEQ ID NO 25; 41pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                 98US-0093685P.
99US-00359268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.4%;
                                                                                                                                                                            Dinman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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Pred.
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The invention relates to a method of identifying a test composition that modulates the efficiency of translation termination comprising contacting

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

WPI; 2004-061375/06

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ARSSULT 7
ANDS23757
ID ADS23
XX
AC ADS2
XX
XX
RECC
DR Bact
XX
Recc
XW Coold
KW path
KW path
KW bact
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IS20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                  (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial polypeptide #12790.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RNA helicase MTT1 with a composition or agent under conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493
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                                                                                                                                                                                                                                                                                  HINKLE G
SLATER S
CHEN X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorus; photosynthesis; lignin; galactomannan;
polypeptide.
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                                                                                                                                                                                                                                                                                                                   9.5
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                                                                                                                                                                                          SC,
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Pred. No. 1.9e-05;
1; Mismatches 2
                                                                                                                                                                                          Chen
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                                                                                                                                                                                             Goldman
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promoter functional in a plant cell, where the promoter is positioned provide for expression of a polynucleotide encoding a polypeptide from

Claim 1; SEQ

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NO 12790; 122pp; English.

invention

relates

6

recombinant DNA

construct comprising

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ADN19868
ID ADN19868
ID ADN19868
ID ADN19868
AC ADN1
XX ADN1
XX ADN1
XX ADN1
XX Bact
XX Recc
XW Cold
KW Cold
KW Cold
KW Dath
KW Dath
XX Dath
XX Dath
XX Dath
XX Dath
XX ISA
DA GOL
XX GAC
A GAC

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogen tolerance; pest tolerance; plant under tolerance; pathogen tolerance; pest tolerance; plant growth regulator; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN19868 standard; protein; 1944 AA
                                                                                                 (HINK/)
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                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003US-00369493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria
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                                                                                                                                                                    (CAOY/)
                                                               CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718
                                 HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IGFLXDXRRINVALTRAK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorus; photosynthesis;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide #2521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 73; DB
; Pred. No. 5.2e
1; Mismatches
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. 5.2e-05;
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0

Query Match

Length 1944;

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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polymucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC such as maize or soybean. The method of producing a plant with the recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to harbicides, extreme osmotic conditions, pathogens or pests, colerance to plant disease, better growth rate by modification CC of the cell cycle pathway with plant growth regulators, increased rate of the monologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production of the protosynthesis or by condition, improved plant growth and development under at least one stress condition, improved lignin production of the protosynthesis or by production. This sequence represents a bacterial polypeptide used in the grope of the invention. Note: The sequence data for this patent did not form part form lugary are secretal untro.
Sequence 1944 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                        from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinkle GJ,
                                                      at segdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
Matches
                                                                                                                                                Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                             Human ORFX protein sequence SEQ ID NO:15322.
                                                                                                                                                                                                                                                       25-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                ABP07670
                                                                                                                                                                                                                                                                                                        ABP07670 standard; protein;
                                                                                                                                       mmune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                      1729
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                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              IGFLXDXRRINVALTRAK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     92.4%;
83.3%;
                                                                                                                                                                                                                                                                                                         98
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Pred. No. 0.00011;
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29-MAY-2001; 2001WO-US010836.

06-DEC-2001.

myasthenia gravis.

autoimmune disorder;

rheumatoid

autoimmune thyroiditis

Homo sapiens.

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ARESULT 10
AAY77815
ID AAY77
XX
AC AAY77
XX
DT 31-MA
XX
Peast
XX
Helic
KW Helic
KW Helic
KW betar
KW betar
KW helic
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Sacch
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PN WO200
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PD 03-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemornhage, costeoarthritis, neurodegenerative disorders disorders related to organ cost transplantation, cardiovascular diseases, diabetes mellitus, systemic clupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, concedegenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic commune the protection of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                    Helicase B; HCSB; MTT1; modulator of translation termination; eRF1; eukaryotic release factor; peptidyl transferase; beta-thalassemia; beta-globin; Duchene/Becker Muscular Dystrophy; antianemic; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                 Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                       31-MAY-2000
                                                           WO200005586-A2
                                                                                                                                                                                                                                 Yeast Senl
                                                                                                                                                                                                                                                                                                                                              AAY77815 standard; peptide; 471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 15322; 1037pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (referred to as open reading frame, ORFX, where X is 1-11491 (see in the specification). ABN15762 to ABN27252 encode the human ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGFLXDXRRINVALTRAK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                             IGFLSDSRRLNVALTRAR
                                                                                                                                                                                                                               protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes substantially purified human reading frame, ORFX, where X is 1-11491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB Pred. No. 6e-0 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table
                                                                                                                                                                                            eRF3;
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RESULT 11 ABW01202

ABW01202 standard; protein; 472

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454

1 IGFLXDXRRINVALTRAK 18

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VGFLKDFRRMNVALTRAK 471

TX SX FX BX BX BX SX S

15-JAN-2004 ABW01202

(first entry

Saccharomyces cerevisiae

therapy; HCSB; nonsense mutation; yeast

Modulator of translation termination; MTT1; helicase

B; antiviral;

cerevisiae SEN1 protein.

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CC carry out translation termination in eukaryotic cells, peptidyl
CC eukaryotic release factor (eRP) 1 and eRP3. The complex can be used to
CC modulate peptidyl transferase activity during translation in a cell. It
CC can be administered therapeutically combined with a carrier in
CC pharmaceutical compositions to treat diseases associated with peptidyl
CC transferase activity, especially diseases associated with peptidyl
CC transferase activity, especially diseases resulting from a nonsense or
CC Muscular Dystrophy etc. It can be used to identify disease conditions
CC involving a defect in the complex, by transfecting cells with encoding
CC and after transferase activity during translation, inhibiting the
CC peptidyl transferase activity during translation, inhibiting the
CC interaction between MTI and eRP3 or involved in enhancing translation
CC termination. Vectors comprising polymucleotides encoding the complex of
CC interfere with complex expression and so modulate the efficiency of
CC translation termination of mRNA and/or degradation of aberrant
Matches
                    Query Match
Best Local 9
                                                                                                                                                                  transcripts in a cell. Agents binding to the complex can be identified and included in therapeutic compositions useful as above, and/or used to modulate peptidyl transferase activity during translation in cells. They are also useful to modulate the efficiency of translation termination of mRNA at a nonsense codon and/or promote degradation of aberrant transcripts in cells. The method can be used to identify agents/compositions modulating binding to MTT1, useful to identify genes.
                                                                                   Sequence
                                                                                                                            Sequences AAY77813-817
group I helicases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translation Termination) and the conserved proteins known to interact and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidyl transferase activity during translation. The complex comprises the gene encoding Helicase B (HCSB; renamed MTT1, for Modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferase activity e.g. Duchene/Becker Muscular Dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New multiprotein complex which can modulate peptidyl transferase activity during translation, useful to treat diseases associated with peptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNE-) UNIV NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention provides a new multiprotein complex which can modulate
14,
                      Similarity
                                                                                     471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Czaplinski K,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US016802
                    89.9%;
77.8%;
                                                                                                                                                  represent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dinman
<u>ب</u>
                    Score 71; DB 3;
Pred. No. 5.5e-05;
    Mismatches
                                                                                                                                                fragments
  2
                                        Length 471;
                                                                                                                                                     from
                                                                                                                                                  yeast superfamily
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Gaps
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; translation termination; RNA helicase; MTT1; frameshift frequency; aberrant transcript degradation; peptidyl transferase modulation; beta-thalassaemia; beta-globin; puchenne/Becker Muscular Dystrophy; Haemophilia B; Von Willebrand Disease; Osteogenesis Imperfecta; Breast cancer; Ovarian Cancer; Wilms Tumour; Hirschsprung disease; Cystic fibrosis; Kidney Stone; Familial hypercholesterolaemia; Retinitis Pigmentosa; Neurofibromatosis; Retinoblastoma; ATM; Costmann Disease; yeast; enzy
(PELT/)
(CZAP/)
(DINM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying an agent that increases nonsense suppression, for anti-
therapy, by contacting modulator of translation termination (Mtt1)
Saccharomyces cerevisiae with a test agent, and detecting specific
binding to Mtt1.
                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast helicase Senl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of identifying an agent that increases nonsense suppression, by contacting modulator of translation termination (MTT1) also referred to as helicase B (HCSB) in Saccharomyces cerevisiae. The method is useful for identifying compositions or agents which increase nonsense suppression. The invention may also be used for antiviral therapy and for suppression of pathological nonsense mutations. The present sequence is Saccharomyces cerevisiae SEN1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-810549/76
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                                                                                                           22-JUL-1998;
22-JUL-1999;
                                                                                                                                                                                          28-AUG-2003; 2003US-00652334.
                                                                                                                                                                                                                                                   17-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 VGFLKDFRRMNVALTRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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) PELTZ S.
) CZAPLINSKI K.
) DINMAN J D.
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                                                                                                           98US-0093685P
99US-00359268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dinman JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB
Pred. No. 5.5e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; ...
5.5e-05; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                  yeast; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of identifying a test composition that combodiates the efficiency of translation termination comprising contacting the RNA helicase MTTI with a composition or agent under conditions comparising contacting contacting the RNA helicase MTTI with a composition or agent under conditions composition and methods are useful for modulating the MTTI. The composition and methods are useful for modulating the fidelity of composition and methods are useful for modulating that: affect the composition and methods are useful for modulating that: affect the composition and methods are useful for modulating that: affect the composition and methods are useful for modulating that: affect the composition and civity of maNAs by altering frameshift frequency, permit composition activity of maNAs by altering frameshift frequency, permit committees and provide modulators (inhibitors/stimulators) of peptidyl transcripts, and provide modulators (inhibitors/stimulators) of peptidyl cranscripts, and provide modulators (inhibitors/stimulators) of peptidyl cransfersse activity during initiation, elongation, termination and maNA comparation of translation. The agents, which may be antagonists or composition of constance useful in screening, diagnostic and therapeutic purposes, composits, are useful in screening, diagnostic and therapeutic purposes, composition, and managential permit and therapeutic purposes, constance beta-chalasseemia, beta-globin, buchemne/Becker Muscular constance of the sequence, or well-brand Disease, Cystic fibrosis, Kidney Stones, Pamilial Tumour, constance of the yeast helicase Seni.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                   EP1258494-A1.
                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                           Protein sequence #SEQ ID 1767
                                                                                                                                                                                                                                                                                                                                                               20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                   ABR53451;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR53451 standard; protein; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a test composition or agent that modulates the efficiency of translation termination comprises contacting the MTT1 with the test composition or agent, and determining if the test composition or agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peltz S,
                                                                                                       15-MAY-2001; 2001EP-00111774
                                                                                                                                         20-DEC-2001; 2001BP-00130253.
                                                                                                                                                                               20-NOV-2002.
                                                                                                                                                                                                                                                                                       Multiprotein complex; eukaryote; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibits the MTT1.
                                                                     (CELL-) CELLZOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IGFLXDXRRINVALTRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGFLKDFRRMNVALTRAK
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 472;
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Bauer A, G Marzioch M,

Gavin A, Gran M, Schultz JD,

Grandi P,

i P, Krause R, K Superti-Furga GD;

Kruse UD,

Kuester BD;

N-PSDB;

ACC61493.

2003-250078/25

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RESULT 14
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      REAL AND COURT OF THE PARK SON COURT OF THE 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                   Bauer A, Ga
Marzioch M,
                                                                                                                                                                                                                                                                    WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                 New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-2002; 2002EP-00102902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CELL-)
      invention relates to
                                                                                                                                                                                                                                                                       2003-638460/61.
DB; ADK64623.
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                                                                                                                                                                                                                                                                                                                                                           Gavin A, Superti-Furga G, Kuester B, Som, Grandi P, Krause R, Kruse U, Merino Leutwein C, Rick J;
                                                          SEQ ID NO 2127; 13pp; English.
                                                                                                                        a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug target; diagnosis
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77.8%;
novel protein complexes comprising a first
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Pred. No. 0.00028;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Schultz J;
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Claim 1;

SEQ ID

NO 1830; 122pp; English

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

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RESULT 15
ADN19177
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               nitrogen;
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator;
                                                                                                                                                                                         (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial polypeptide
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                                                                                                           WPI; 2004-061375/06
                                                                                                                                          Cao Y,
                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     second protein, or its derivative, fragment, homologue or variant.
                                                                                                                                                                        (GOLD/)
                                                                                                                                                                                                                                         (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nomologous recombination; seed oil
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                                                                                                                                                                        GOLDMAN B
                                                                                                                                                                                          CHEN X
                                                                                                                                                                                                                                         CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorus; photosynthesis;
polypeptide.
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Pred. No. 0.00028;
                                                                                                                                          Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                              lant growth regulator;
yield; protein yield; carbohydrate;
is; lignin; galactomannan;
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                                                                                                                                            Goldman
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CC The invention relates to a recombinant DNA construct comprising a CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC microbial source. The invention also relates to a transformed plant CC transformed plant thaving an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transformed plant with the CC recombinant DNA construct and growing the transformed plant with the CC improved plant but construct is useful for improving plant properties. CC The recombinant DNA construct is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, colding plant properties, e.g. improved cold, heat or drought tolerance, coldinare to herbicides, excreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or consophorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan cc condition. Note: The sequence data for this patent did not cf form part of the printed specification but was obtained in electronic cc format from USPTO at segdata.uspto.gov/sequence.html. Sequence 2231 AA; y Match 89.9%;
Local Similarity 77.8%;
hes 14; Conservative 2 Score 71; DB 8; Length 2231; Pred. No. 0.00031; 2; Mismatches 2; Indels 0 Gaps 0

Search completed: April 18, 2005, 08:03:51 Job time : 89.717 secs 밁 গ Query Match Best Local S Matches

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Result
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DB
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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79
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    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                US-09-359-268A-9
US-09-248-796A-19347
US-09-248-796A-19347
US-09-248-796A-19107
US-09-248-796A-19107
US-09-270-984A-4
US-09-270-984A-2
US-09-270-984A-2
US-09-29-268A-29
US-09-29-268A-29
US-09-270-767-44429
US-09-359-268A-24
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Compugen Ltd
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e 26, Appli
e 4, Appli
e 4, Appli
e 2, Appli
e 10116, A
e 16148, A
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25, Appl
19347, A
19107, A
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RESULT 2 US-09-359-268A-25 J. Sequence 25, Application US/09359268A PATENT NO. 6630294 GENERAL INFORMATION: APPLICANT: Peltz, Stuart APPLICANT: Czaplinski, Kevin APPLICANT: Cimman, Jonathan D. TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 601-1-85N CURRENT APPLICATION NUMBER: US/09/359,268A CURRENT FILING DATE: 1999-07-22 PRIOR APPLICATION NUMBER: 60/093,685	Query Match 94.9%; Score 75; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 3.5e-08; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 IGFLXDXRRINVALTRAK 18	RNA HELICASES WHICH OF TRANSLATION TERMINA 159,268A	28 47 59.5 181 4 US-09-270-767-47055 Sequence 47055, A 29 46 58.2 219 4 US-09-270-767-56745 30 46 58.2 238 4 US-09-270-767-56745 Sequence 56745, A 31 46 58.2 486 4 US-09-270-767-41521 Sequence 56745, A 32 44 55.7 2108 4 US-09-252-991A-31502 Sequence 31502, A 33 41 51.9 345 4 US-09-252-991A-31502 Sequence 13564, A 34 49.4 426 4 US-09-202-540-13564 Sequence 13564, A 35 39 49.4 426 4 US-09-902-540-12700 Sequence 12700, Ap 36 39 49.4 1213 4 US-09-902-540-12700 Sequence 10712, A 37 38 48.1 1233 4 US-09-489-039A-10712 Sequence 6478, Ap 39 37 46.8 177 2 US-08-700-013B-11 Sequence 46729, App1 40 37 46.8 177 2 US-08-700-013B-11 Sequence 11, App1 41 37 46.8 251 4 US-09-191-468-76 Sequence 72, App1 43 37 46.8 251 4 US-09-191-468-76 Sequence 74, App1 44 37 46.8 251 4 US-09-191-468-78 Sequence 75, App1 55 37 46.8 251 4 US-09-191-468-78 Sequence 76, App1 56 37 46.8 251 4 US-09-191-468-78 Sequence 78, App1 57 46.8 251 4 US-09-191-468-78 Sequence 78, App1
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US-09-248-796A-19347
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SEQ ID NO 25
LENGTH: 415
                                                                                                                                                                       Sequence 19107, Application US/09248796A
Patent No: 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PELING DATE: 1998-02-13
PRIOR PELING DATE: 1998-08-13
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SEQ ID NO 19347
LENGTH: 917
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SEQ ID NO 19107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Baccharomyces cerevisiae
                    NAME/KEY: UNSURE
                                                                          ORGANISM: Candida albicans
MTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 15; Conserv
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83.3%;
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83.3%;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 26
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6630294 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Applia Patent No. 599411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09359268A
            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dietz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMII
TITLE OF INVENTION: THE FIDELITIES OF INVENTION: THEREOF
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APPLICANT: Czaplir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: saccharomyces cerevisiae
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TYPE: PRT
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MAMMALIAN REGULATO TITLE OF INVENTION: NONSENSE-MEDIATED
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                      CITY: La Jolla
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson, STREET: 4225 Excutive Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 VGFLKDFRRMNVALTRAK 472
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                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                   Dietz, Harry C.
VENTION: MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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77.8%;
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77.8%; Pred. No. 9
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Pred. No. 4.8e-06;
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Suite 1400
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Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09270984A Patent No. 6048965 GENERAL INFORMATION:
                                                           Matches
                                                                                      Query Match
                                                                                                                                                                                          TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE JOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1043 amino acids
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: WI
                                                                                                                                  TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson, P.C.
STREET: 4225 Excutive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                          Local Similarity
                                                                                                                                                                                LENGTH:
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                                                           14;
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GY: linear
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GY: linear
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               IGFLXDXRRINVALTRAK 18
                                                                                                                                                                                1043 amino acids
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NVENTION: MAMMALIAN REGULATOR OF
NVENTION: NONSENSE-MEDIATED RNA DECAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                           Conservative
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                                                                                                                                  protein
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                                                                          87.3%;
77.8%;
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                                                           <u>ب</u>
                                                                          Score 69; DB 3;
Pred. No. 5.6e-05;
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Pred. No. 5.
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                        DB 3; Length 1043;
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US-08-724-354D-2
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Patent No. 6048965

GENERAL INFORMATION:

GENERAL TOANT: Dietz, Harry C.

MAMMAL
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FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL C.
GENE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                       ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: li
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson, P.C. STREET: 4225 Excutive Square, Suite 1400
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                                                                                                                                                                                                                                                                La Jolla
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4225 Excutive Square, Suite 1400
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                                                                                                                                     Diskette
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77.8%;
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Pred. No. 6e-05;
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US-09-902-540-16148
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US-09-949-016-10116
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Best Local Similarity 77.8
                        APPLICANT: Goldman, E
APPLICANT: Hinkle, G
APPLICANT: Slater, S
APPLICANT: Wiegand,
                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 10116
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Patent No. 681233
                                                                                                             Sequence 16148, Apparent No. 6833447
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
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LENGTH: 1118 amino acids
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
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                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                872 IGFLNDPRRLNVALTRAR 889
                                                                                                                                                                                                                                                                               l Similarity 77.0
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                      Slater, Steven C. Wiegand, Roger C.
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                                                        Barry S.
Gregory J.
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77.8%;
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Pred. No. 6e-05;
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Best Local Similarity
Thes 13; Conserve
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US-08-724-354D-22
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16148
LENGTH: 211
                                                                                                                                                                                                                                                         Sequence 22, Application US/08724354D Patent No. 5994119
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/359,268A
CURRENT FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                                    Agent No. J. GENERAL INFORMATION:
GENERAL INFORMATION: HATTY C.
APPLICANT: Dietz, Hatty C.
APPLICANT: NUTRITION: MAMMALIAN REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan
TITLE OF INVENTION: A SUBPAM
TITLE OF INVENTION: THE FIDE
TITLE OF INVENTION: THEREOF
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SOFTWARE: PatentIn V
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              ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                    NUMBER OF SEQUENCES: :
                                                                STATE: C.
                                                                                                ADDRESSEE: Fish & Richardson,
STREET: 4225 Excutive Square,
CITY: La Jolla
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                               363
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IBM Compatible
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77.8%;
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Pred. No. 2.8e-05;
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Pred. No. 1.4e-05;
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Suite 1400
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RESULT 14
US-09-270-984A-22
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US-09-270-984A-22
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                                            TELEPAX: 619-07-0 2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 01-OCT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Halle, Liea A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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              TOPOLOGY: 1:
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STREET:
TTY: La Ju-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                           amino acid
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77.8%;
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Pred. No. 8.1e-05;
1; Mismatches 3
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Search completed: April 18, 2005, 08:18:37 Job time: 23.4672 secs
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; FRAGMENT TYPE:
US-09-177-431-8
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Patent No.
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Best Local Similarity
                                                                                                                          Matches
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: PastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0791
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                  TELEFAX: 01.
                                                                                                                                                                                                                                 LENGTH: 971 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Pred. No. 8.1e-05;
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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79
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13	12	11	10	9	8	7	6	ហ	4	w	N	_	Regult No.
70	70	70	70	70	70	70	71	71	73	73	73	75	Score
88.6	88.6	88.6	88.6	88.6	88.6	88.6	89.9	89.9	92.4	92.4	92.4	94.9	Query
656	655	653	650	648	439	123	2231	472	1944	992	415	18	Query Match Length DB
15	16	15	15	15	16	15	15	16	15	15	16	16	8
US-10-369-493-1268	US-10-828-924-80	US-10-369-493-21645	US-10-369-493-2884	US-10-369-493-20334	US-10-767-701-41078	US-10-424-599-216889	US-10-369-493-1830	US-10-652-334-26	US-10-369-493-2521	US-10-369-493-12790	US-10-652-334-25	US-10-652-334-9	ID
Sequence 126	Sequence 80,	Sequence 216	Sequence 2884,	Sequence 203:	Sequence 410	Sequence 2168	Sequence 183	Sequence 26,	Sequence 252:	Sequence 1279	Sequence 25, Appl	Sequence 9, Appl	Description
1268, Ap	80, Appl	21645, A	4, Ap	20334, A	41078, A	216889,	1830, Ap	26, Appl	2521, Ap	12790, A	App1	Appli	;

20	63 79.	63 79.	63 79.	64 81.	66 83.	66 83.	66 83.	66 83.	. 66 83.	66 83.	66 83.	66 83.	67 84.	67 84.	67 84.	67 84.	67 84.	67 84.	67	67 84.	67 84.	68 86.	69	69 87.	69 87.	69 87.	69 87.	69 87.	16 69 87.3	69 87.
890	639	637	317	693	1323	1027	626	404	350	332	215	127	1975	663	648	642	611	250	182	161	88	380	1361	1118	935	925	734	638	449	
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-10-437-	-10-425-1	-10-424-599-	-10-425-1	-10-369-4	0-437-9	-10-437-963	-10-437-963	0-425-114	-10-424-5	-10-425-1	-10-425-1	-10-767-	0-437-9	-10-369-493	-10-369-493	US-10-369-493-21526	-10-369-493	-10-424	-10-767-701-	-10-425	-10-437	-10-652	-10-437-963-	-10-474-553-	-10-408-76	-10-369-493	-10-424-599	63-18169	-10-425-114-5776	-10-425-114-4285
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	ø	ø	Ф	æ	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
118530,	37717, A	233501,	•	5272, Ap	11794	185291,	6632	7833	41211,	7,	2518,	48804, A	140079,	•		21526, A	۳	ŭ	,	38303, A		29, Appl	165703,	6, Appli	1706, A	2087, Ar	205643,	816		285

ALIGNMENTS

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RESULT 1

US-10-652-334-9

Sequence 9, Application US/10652334

Publication No. US20040115787A1

GENERAL INFORMATION:

APPLICANT: Peltz, Stuart

APPLICANT: Czaplinski, Kevin

APPLICANT: Dinman, Jonathan D.

TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES TITLE OF INVENTION: THE FOLLITY OF TRANSLATION TERMINATION AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 601-1-85N

CURRENT APPLICATION NUMBER: US/10/652,334

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US/09/359,268A

PRIOR FILING DATE: 1999-07-22

PRIOR FILING DATE: 1998-07-22


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                                                                                              Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
                                                                                                                                                                                                                    TYPE: PRT
ORGANIM: saccharomyces cerevisiae
FEATURE:
OTHER INFORMATION: Kaa = any amino acid
                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                              l Similarity
18; Conserv
IGFLXDXRRINVALTRAK 18
                            IGFLXDXRRINVALTRAK 18
                                                                                         94.9%; Score 75; DB 16; llarity 100.0%; Pred. No. 6.6e-08; Conservative 0; Mismatches 0;
                                                                                                                                                Length 18;
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RESULT 4
US-10-369-493-2521
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US-10-652-334-25
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                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Aspergillus nidulans
US-10-369-493-12790
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PRILING DATE: 2002-02-21 NUMBER: OF SEQ ID NOS: 47374 SEQ ID NO 12790 LENGTH: 992
TYPE: PRT
Sequence 2521, Application US/10369493 Publication No. US20030233675A1
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Best Local
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Publication No. US20040115787A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
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APPLICANT: Czaplinski, Kevin
APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 601-1-85N
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Local Similarity 83.3%;
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es 15; Conservative
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18 IGFLSDPRRLNVALTRAK 735
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83.3%;
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Pred. No. 1.6e-05;
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RESULT 6
US-10-369-493-1830
y Sequence 1830, Application US/10369493
publication No. US20030233675A1
representation:
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CURRENT APPLICATION NUMBER: US/10/652,334
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/09/359,268A
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/093,685
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.0
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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LENGTH: 1944
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Czaplinski, Kevin
APPLICANT: Dinman, Jonathan D.
APPLICANT: Dinman, Jonathan D.
TITLE OF INVENTION: A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS
TITLE OF INVENTION: THE FIDELITY OF TRANSLATION TERMINATION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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Pred. No. 1.8e-05;
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Pred. No. 3.5e-05;
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APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S.

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US-10-369-493-1830
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1830
LENGTH: 2231
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216889
LENGTH: 123
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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NAME/CRY: unsure
LOCATION: (1)..(123)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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72.2%;
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77.8%;
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Pred. No. 0.0001;
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      ORGANISM: Thermotoga maritima
                                           ENGTH:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory G.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2884
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LENGTH: 439
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Publication No. US20030233675A1
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Best Local (
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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ORGANISM: Sorghum bicolor
FEATURE:
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Pred. No.
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Pred. No. 2.6e-05;
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                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Helicase
US-10-828-924-80
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-828-924-80
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 80, Application US/10828924
Publication No. US20050003401A1
GENERAL INFORMATION:
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Best Local
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SEQ ID NO 21645
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                                                                                                                                                                                                                                                                                                         APPLICANT: STRATAGENE
TITLE OF INVENTION: PUR REPLICATION ACCESSORY FACTORS AND METHODS OF USE
FILE REFERENCE: 04121.0161-00000
CURRENT APPLICATION NUMBER: US/10/828,924
CURRENT FILING DATE: 2004-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: EXCRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-369-493-21645
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/146,580 PRIOR FILING DATE: 1999-07-30
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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Pred. No.
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Pred. No. 4.1e-05;
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
FITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT TILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 45987
LENGTH: 415
TYPE: PRT
ORCANT-
RESULT 15
US-10-425-114-42857
; Sequence 42857, Application US/10425114
; Publication No. US20040034888A1
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US-10-369-493-1268
                                                                                                                                                                                                                                                     US-10-425-114-45987
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SEQ ID NO 1268
LENGTH: 656
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US 60/369,493
CURRENT FILING DATE: 2003-02-28
BRIOR APPLICATION UNMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: 700842952_FLI.pep
                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
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Pred. No.
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Pred. No. 3.8e-05
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GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42857
LENGTH: 437
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INVORMATION: Clone ID: 700476463_FLI.pep
US-10-425-114-42857
Query Match
Best Local Similarity 77.8t; Pred. No. 4.1e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Matches 14: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OTHER INVOLTERAN 18

Search completed: April 18, 2005, 09:04:08

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A;Molecule type: DNA
A;Residues: 1-1121 <DIE>
A;Residues: 1-1121 <DIE>
A;Crobb-references: EMBL:U18922; NID:g603405; PIDN:AAB64703.1; PID:g603417; MIPS:YER176w
A;Crobb-was, E.E.; Chen, P.H.; Lebsyk, J.; Biswas, S.B.
Biochem. Biophys. Res. Commun. 206, 850-856, 1995
A;Title: Biochemical and genetic characterization of a replication protein A dependent D.
A;Reference number: JC2490; MUID:95134267; PMID:7832796
A;Accession: JC2490.
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 09-Jul-2004
C;Accession: S30862; 850679; 702490; PC2368
C;Accession: J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
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                                                                                                                                                                                                    A;Cross-references: SGD:S0000978; MIPS:YER176w
A;Map position: SR
C;Keywords: nucleotide binding; P-loop
P;670-677/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 277-283;623-633,'X',635-643 <BI2>
C;Comment: This enzyme plays pivotal roles in
                                                                                                                                                                                                                                                                                                               A;Gene: SGD:ECM32
                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1121 <BIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the RMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 9163 and 9132.
A; Reference number: S50679
A; Accession: S50679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P32644; GB:U18922; EMBL:L11229; NID:g603405; PIDN:AAB64703.1
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A; Residues: 1-1121 < MUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: PC2368
                                                                                                  Matches
                                                                                                                                                   Query Match
                                                                                                                             ocal
1065
                                                                                                  15;
                              1 IGFLXDXRRINVALTRAK 18
                                                                                                                                Similarity
IGFLRDKRRLNVALTRAK 1082
                                                                                                     Conservative
                                                                                                                        92.4%;
83.3%;
                                                                                                  <u>ب</u>
                                                                                                                             Score 73;
Pred. No.
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                                                                                                       Mismatches
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                                                                                                  73;
No. 1.4e-05;
                                                                                                                                                      DB 2;
                                                                                                                                                      Length 1121;
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RESULT 2

tRNA-splicing endonuclease positive effector - fission yeast (Schizosaccharomyces pombe)

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C;Accession: T40065
R;Lyne, M.; Rajandream, M.A.;
submitted to the EMBL Data Lik
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E90113
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A; Molecule type: DNA
A; Residues: 1-1944 < LYN>
A; Cross-references: UNIPROT: 094387; EMBL: AL034463;
A; Cross-references: strain 972h-; cosmid c29A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revisic
C;Accession: T40065
                                                                                                                             A;Title: SMG-2 is a phosphorylated protein A;Reference number: Z22389; MUID:99384262; A;Accession: T43280
                                                                                                                                                                                      R; Page, M.F.; Carr, B.; Anders, Mol. Cell. Biol. 19, 5943-5951,
                                                                                                                                                                                                                           C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change C;Accession: T43280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein component of a tRNA splicing complex [imported] - Guil: C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                            A; Molecule type: mRNA
                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                nonsense-mediated mRNA decay trans-acting factor - Caenorhabditis elegans C_1:Species: Caenorhabditis elegans
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A; Residues: 1-692 < DOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 410, 1091-1096, 2001
A;Title: The highly reduced
A;Reference number: A99082;
A;Accession: E90113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Nature 410, 1091-1096, 2001
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A; Accession: T40065
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Best Local S
Matches 15
                                                        Cross-references:
                 Query Match
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Best Local
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                                                      UNIPROT:076512; EMBL:AF074017; NID:g3328176; PIDN:AAC26789.1;
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83.3%;
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83.3%;
                   89.9%;
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                                                                                                                                                                                      K.R.; Grimson, A.; Anderson, 1999
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Pred. No. 1.3e
0; Mismatches
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Pred. No. 2.4e-05;
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                   71;
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1.3e-05;
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                 Length 1069;
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A;Status: r---
A;Nolecule type: DNA
A;Residues: 1-245 <ARN>
A;Cross-references: UNIPROT:Q9X1D1;
A;Cross-references: strain MSB8
                                                                                                         A;Experimental source: C;Genetics: A;Gene: TM1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: may be component of nuclear splicing complex C;Keywords: nucleotide binding; nucleus; P-loop F;1357-1364/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: DNA
A;Residues: 'MHS',130,'FCEREVQ',131-2231 <DEM>
A;Residues: 'MHS',130,'FCEREVQ',131-2231 <DEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ric
                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: D72258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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R;deMarini, D.J.; Winey, M.; Ursic, D.; Webb, F.; Culbertson, M.R.
Mol. Cell. Biol. 12, 2154-2164, 1992
A;Title: SENI, a positive effector of tRNA-splicing endonuclease in A;Reference number: A44387; MUID:92236590; PMID:1569945
A;Accession: A44387
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submitted to the EMBL Data Library, February ביים שאם המונים February ביים שאם המונים המונים המונים ביים המונים המונים ביים המונים המונ
                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S53416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Title:
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88.6%;
77.8%;
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77.8%;
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Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.8e-05;
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(AB972)
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                                                                                                                                                                                                                              GB:AE001793; GB:AE000512; NID:g4981963; PIDN:AAD36482
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70;
No.
   DB 2;
1.1e-05;
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Local Similarity

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RESULT 9
B75105
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C;Superfamily: probable DNA helicase MJ0104
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72429
probable DNA helicas PAB1561 - Pyrococcus abyssi (strain Orsay) (;Species: Pyrococcus abyssi (;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change C;Accession: B75105
                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: G72429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: D70476
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                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-650 < ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
;Accession: D70476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references:
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ce: strain VF5
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77.8%;
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77.8%;
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Pred. No. 2.4e
2; Mismatches
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                                                                                                                                                                                                      Pred. No. 2.9
?; Mismatches
                                                                                                                                                                                                                                                                                                                                          GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD3509
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                                                                                                                                                                                                                      DB 2;
2.9e-05
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               #text_change 09-Jul-2004
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                             A; Gene: SPDB:Sr/
A; Map position:
                                                                    A; Experimental source: strain C; Genetics:
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Query Match

88.6%;

Score

70;

DB 2

Length 1687;

SPDB:SPAC6G9.010c

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C; Accession: T39072
R; Murphy, L; Harris,
submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: this accession replaces C;Genetics:
A;Gene: PH0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: E71080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Ohfuku, Y.; Funahashi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Pyrococcus abyssi genome
A;Reference number: A75001
A;Accession: B75105
A;Status: preliminary
                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1687 <MUR>
                                                                              A; Reference number: Z21825
A; Accession: T39072
                                                                                                                                                          DNA2-NAM7 helicase family protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable DNA-binding protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug_1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
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               A;Cross-references: UNIPROT:Q92355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 14-Au
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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C;Superfamily: probable DNA helicase MJ0104
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A; Residues: 1-653 < KAW>
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                                                                                                                D.; Barrell, B.G.; Rajandream, M.A.;
Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                  88.6%;
                                                                                                               Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horikawa, H.; Haikawa, Y.; Hino, Y.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                    Score 70; DB
Pred. No. 3e-(
2; Mismatches
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Pred. No. 2.9e-05;
                                                                from
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                                                                                                               August
EMBL: Z81317; cosmid c6G9
                                                                  GB/EMBL/DDBJ
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3e-05;
                 PIDN: CAB03612.1;
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                 GSPDB:GN00066;
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Kushida, N
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                   SPDB:SP
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Oguchi
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D86303
                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q09820; EMBL:Z54366; NID:g1019812; PIDN:CAA91194.1; PID:g132R,Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995
A;Reference number: Z21745
A;Accession: T37779
                                                                                                                                     A;BCENTUS. F-----
A;NOlecule type: DNA
A;Residues: 11-935 <BA2>
A;Residues: 11-935 <BBL:Z54366; PIDN:CAA91194.2; GSPDB:GN00066; SPDB:SPAC16C9.06c
A;Cross-references: EMBL:Z54366; PIDN:CAA91194.2; GSPDB:GN00066; SPDB:SPAC16C9.06c
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A;Residues: 1-2142 <STO>
A;Cross-references: UNIPROT:Q9FWR3; GB:AE005172; NID:g9954728; PIDN:AAG09081.1; GSPDB:GN
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A;Molecule type: DNA
A;Residues: 1-935 <BAD>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Schizosaccharomyces pombe;Date: 16-May-1996 #sequence_revision 13-Mar-1997;Accession: S62476; T37779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: S62445
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Best Local (
                                                              Query Match
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>sition: 1L
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                       14;
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                       Conservative
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                                         87.3%;
77.8%;
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                  Score 69; DB 2; LC
Pred. No. 6.7e-05;
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Pred. No. 0.0001;
2; Mismatches
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                                                              Length 935;
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Query Match
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A;Cross-references: UNIPROT:P30771; EMBL:X62394; NID:g4022; PIDN:CAA44266.1; PID:g4023 R;Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R. M.R. Mol. Cell. Biol. 12, 2165-2177, 1992 Mol. Cell. Biol. 12, 2165-2177, 1992 A;Title: Gene products that promote mRNA turnover in Saccharomyces cerevisiae. A;Reference number: A44388; MUID:92236591; PMID:1569946
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J. Mol. Biol. 224, 575-587, 1992

A;Title: NAM7 nuclear gene encodes a novel member of a family of helicases with a Zn-ligate and the control of the cont
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A;Residues: 1-1311 <BEV>
A;Residues: 1-1311 <BEV>
A;Cross-references: UNIPROT:Q9SZW3; EMBL:ALO78464; GSPDB:GN00062; ATSP:F6G3.130
A;Experimental source: cultivar Columbia; BAC clone F6G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Gentles, S.; Bowman, S. submitted to the EMBL Data Library, May 1995
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A; Accession: T08986
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                                                                                                                                                                                                                                                                                        A;Gene: SGD:NAM7; UPF1
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080c
A;Experimental source: strain AB972
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A;Residues: 1-971 <ALT>
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;Keywords: GTP binding; mitochondrion; nucleotide binding; nucleus; P-loop;430-437/Region: nucleotide-binding motif A (P-loop);545-548/Region: GTP-binding NKXD motif
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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Accession: S23408; A44388; S54455;
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es 13; Conserv
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Pred. No. 9.5e-05;
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Score 68;

DB 2;

Length

밁 Best Local Similarity 77.8%; Pred. No. 0.00011; Matches 14; Conservative 1; Mismatches 3; Indels 1 IGFLXDXRRINVALTRAK 18 |||| ||| |||||| |786 IGFLRDPRRLNVGLTRAK 803 0; Gaps <u>,,</u>

Search completed: April 18, 2005, 08:06:05 Job time: 17.3431 secs

Page 5

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pyrococcus rhodopirell plasmodium

schizosacch

pyrococcus

mus musculu schizosacch

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mus musculu homo sapien

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d. No. is the number of results predicted by chance to have
re greater than or equal to the score of the result being put
is derived by analysis of the total score distribution.
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122.648 Million cell updates/sec
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Endonuclease.

1124 AA;
                                                      Q6C803 PRELIMINARY; PRT; yea Am. Q6C803; Present Control of Contro
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Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
"Paramecium megabase sequencing project.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR548612; CAH03240.1; -.
EMBL; CR548612; F:endonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zagulski M., Nowak J.K., Le Mouel A., N
Gromadka R., Noel B., Blanc I., Dessen
Cohen J., Meyer E., Sperling L.;
"High Coding Density on the Largest Par
Chromosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6BGIO;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
TRNA-splicing endonuclease positive effector, put
ORFNames=PTMB.43c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Stock d4-2;
PubMed=15296759; D
    lipolytica.
ORFNames=YALIOD23881g;
Yarrowia lipolytica CLIB99.
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DOI=10.1016/j.cub.2004.07.029;
DOI=10.1016/j.cub.2004.07.029;
Wincker P., Keller P
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83.3%;
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Q7 ZVZ4
RNT1 MOUSE
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Q8 G225
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Q9epu0
Q6gyp5
Q86z25
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IGFLXDXRRINVALTRAK

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GenCore (c) 1993

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SMART; SMOO487; I
ATP-binding.
ATP-BINDE 964 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosomuses
1140 of Kluyveromyces lactis.
ORFNames=KLLAOROKAZEC.
                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; CR382130; CAG81409.1; -.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR00359; AAA ATPase.
InterPro; IPR011545; DEAD/DEAH_N.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Turkey W. T. Turkey N. Truck B., Groppi A.,
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Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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Wincker P., Souciet J.L.;
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                                                                                                                                                                                                                                                                     Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                       Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharor
Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                          STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=284590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome evolution in yeasts.";
Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00487; DEXDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
      Nikolski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA; 107764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.4%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73; DB 2;
Pred. No. 6.6e-05;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68C05A712597B8DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y-1140 chromosome
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Boisrame A., Boyer J., Cattolico L., Ferry-Dumazet H., Groppi A.,
A Boepons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Boepons L., Febre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Micaud J.M., Noszul R., Lemaire M., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,
A Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
BRA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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Matches
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Query Match
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Q6BPM3;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CR382122; CAH02214.1; -.
InterPro; IPR006935; ResIII.
InterPro; IPR006904; RNA_rec_mot.
Pfam; PF04851; ResIII; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 969 AA; 108943 MW; 208CT4F91B6BCE29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouchier C., Cauchier J.L.;
Souciet J.L.;
Ther P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=DEHAOE13002g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
Debaryomyces hansenii cl
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                                                                                                                                    Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR382337; CAG88086.1; -.
                                                                                                                                                                                                                                                                                                                                           Bouchier C., Caudron B.,
Wincker P., Souciet J.L.
"Genome evolution in yea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                         EMBL; CR382137; CAG88086.1; -.
InterPro; IPR011545; DEAD/DEAH_N.
                                                                                                                                                                                                                            STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                              Nature 430:35-44(2004).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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15; Conserv
                                                       SM00487; DE:
CE 985 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRL Y-1140;
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                                                                                     DEXDc;
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                                                       110705 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.4%;
83.3%;
                                                                                                                                                                                                                                                                                                                                           yeasts.";
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Pred. No. 6.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                          14DBD331A4E37E0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
annotation update)
E of strain CBS767
  73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
  멂
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TFW3;
Q8TFW3;
01-JUN-2002
                                                                                                                                                                                             Knowles D.G., Warren T., Hall N., Quail M., Wo Denning D.W., Anderson M.J., Barrell B.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AL711529; CAD28448.1; -GO; GO:0005524; F:ATP binding; IEA. GO; GO:000166; F:nucleotide binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q75DS7
Q75DS7;
                                                                                                                                                      និនិនិន
                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2004) to the EMBL/GenBa
Submitted (SEP-2004) to the EMBL/GenBa
EMBL; AE016815; AAS50792.2; -.
GO; GO:0000166; F:nucleotide binding;
InterPro; IPR003593; AAA_ATPase.
Pfam; PF04851; ResIII; 1.
SMART; SM00382; AAA; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                   STRAIN=Af293;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashbya gossypii (Yeast) (Eremotnecium g
Eukaryota; Fungi; Ascomycota; Saccharom
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR022Cp.
ORFNames=ABR022C;
                                                                        InterPro; IPR003593; AAA ATPABE.
InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR006935; ResIII.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5085;
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STRAIN=ATCC 10895;
Voegeli S.E., Dietrich
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=33169;
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05-JUL-2004
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                                                                                                                                                 GO:0015668; F:type III site-specific GO:0009307; P:DNA restriction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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i; Ascomycota; Saccharomycotina; Saccharomycetes;
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                 STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maies
Schulte U.;
                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Regulator of nonsense transcripts 1 homolog.
ORFNames=2B4.130, NCU04242.1;
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SEQUENCE
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1060 AA;
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"Insight into the genome of Aspergillus fumigatus: analysis of a kb region encompassing the nitrate assimilation gene cluster.";
Fungal Genet. Biol. 41:443-453(2004).
EMBL; BX649606; CAF32021.1; -.
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PubMed=14998527; DOI=10.1016/j.fgb.2003.12.003;

Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins
Fosker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S.,
O'Neil S., Pertea M., Price C., Rabbinowitsch E., Rajandream M-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation updat 05-JUL-2004 (TremBLrel. 27, Last annotation updat Regulator of nonsense transcripts, putative.
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                                                                                                                                               Neurospora crassa.
Bukaryota; Pungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR011545; DEAD/DEAH_N.
InterPro; IPR006935; ResIII.
Pfam; PF04851; ResIII; 1.
SMART; SM00487; DEXDC; 1.
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Bukaryota; Fungi; Ascomycota; Pezizomycot
Eurotiales; Trichocomaceae; mitosporic Tr
                                                                                                                  SEQUENCE FROM N.A.
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Pred. No. 7.3e-05;
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Pred. No.
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itosporic Trichocomaceae; Aspergillus.
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A Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
A Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
A Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
A Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
A Macceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
A Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
A Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
A Rasmussen C., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A Paulsen C., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
A Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex I.A., Mannhaupt G., Ebbole D.J., Freitag M.,
A Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
The genome sequence of the filamentous fungus Neurospora crassa.";
Nature 422:859-868 (2003)
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ZN FING 111 139
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P32644;
                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
Hypothetical 127.0 kDa protein in RAD24-BMH1 intergenic
OrderedLocusNames=YER176W; ORFNames=SYGP-ORF61;
                                                                                                                                                           YEAST
               Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes,
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EMBL; AABX01000272; EAA31997.1; -.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR001410; DEAD.
TRACTEC. IPR001610; DEAD.
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PubMed=12712197; 1
Saccharomycetales;
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DOI=10.1038/nature01554;
lvo S.B., Borkovich K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.";
. 31:1944-1954(2003).
Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                         92.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ResIII.
                                                                                                                                                                                                                                                                                                                                                           120087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                           M.
                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                              852
                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                        ATP (Poter Poly-Asp.
                                                                                                                                                                                                                                                                                                          Score 73; 1
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-type (atypical)
C4-type (Potential).
ATP (Potential).
                                                                                                                                                                                                                                                                                                                                                 Poly-Asp.
W; 8B0E4F0407ACE142 CRC64;
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential).
Saccharomyces
                                                                                                                                                                                                                                                                                                          DB 1; 1
7.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selker B.U., R
S., Purcell S.,
                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                           Length 1093;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Read N.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Rehman B.,
Endrizzi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aramayo R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n E.L.,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6BNH2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B. Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barl Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruva: Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Leeur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97313264; PubMed-9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A.,
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A.,
Araujo R., Aviles B., Berno A., Brennan T., Carpenter J.,
Cherry J.M., Chung E., Duncan M., Guzman B., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari
Hunicke-Smith S., Namath A., Norgren R.,
Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogre
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indipersion (Indipersion of Charles) (Indipers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Debaryomyces hansenii chromosome B of strain CBS767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00487; DEXDC; 1.
ATP-binding; Helicase; Hypothetical protein.
NP_BIND 670 677 ATP (Potential).
SEQUENCE 1121 AA; 126970 MW; 641C4AA6810282A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genolevures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6BNH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S30862; S30862.
GermOnline; 139253; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the DNA2/NAM7 helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
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GO:0003678; F:DNA helicase
GO:0006449; P:regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGFLXDXRRINVALTRAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB64703.1;
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Pred. No. 7.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            se activity; IDA. of translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1121;
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                                                                                                                                                                                                                  de Daruvar A.,
                                                                                                                                                                                                                                                                                                                    A., Barbe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AC Q6FKP6
DT 05-JU
DT 05-JU
DT 05-JU
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GN ORFN8
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GN ORFN8
OS CANDI
RN [1]
RP SEQUE
RC STRAI
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                                                                                                                                                         Query Match
Best Local S
Matches 15
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ATP-binding.
ATP-binding.
1124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Boffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Boffard N., Frangeul L., Aigle M., Anthouard V., Babour A.,
Barray S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Miller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Miller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Strum M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Neyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome L complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382137; CA888524.1; -. GO:0000166; F:nucleotide binding; IEA. InterPro; IPR003593; AAA, ATPase. InterPro; IPR001547; Glyco_hydro_5. SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., With B., Zeniou.Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.; Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouchier C., Caudron B.,
Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CBS138;
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                                                                                                                                                                                                                                                                                                                                                                                                            Nature 430:35-44(2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1067
                                                                                                                                                                                                                                                                                                                           CR380958;
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IGFLKDORRLNVALTRAK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGFLXDXRRINVALTRAK 18
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                                          Conservative
                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                               CAG62265.1; -.
AA; 127137 MW;
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83.3%;
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                                                                                                                                                         Score 73; DB
Pred. No. 7.76
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                               63C0428123F3CC8C CRC64;
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7.7e-05;
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RESULT 12
Q7RKP6
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Best Local
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; Wood V., Gwilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Stroke K., Brown D., Brown S., Chillingworth T., Churcher C., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamiin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Monley P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AAI
SEQUENCE
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                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                         094387;
                                                                                                                                                                                                                                                                                                                                                                       094387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1236865; DOI=10.1038/nature01099;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
respect D.T., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               Name=SPBC29A10.10c;
                                                                                                                                                                                                                                                                                          SPBC29A10.10c protein.
                                                                                                                                                                                                                                                                                                                                         01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence and comparative analysis parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
                                                                                                                                                                                               NCBI_TaxID=4896;
                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PY02854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: The sequence shown EMBL/GenBank/DDBJ whole genc preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGFLKDERRLNVALTRAK 942
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134154 MW;
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26,
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Last seq
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Last sequence update)
Last annotation update)
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Pred. No. 7.
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notgun (WGS)
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entry v
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Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., RA Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D., RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., The genome sequence of Schizosaccharomyces pombe.";

RI "The genome sequence of Schizosaccharomyces pombe.";

RMBL: AL1014461. "Nature V., Al1014461."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT QBIET99
ID ET99
ID ET99
AC QB
RESULT 15
Q9AVZ7
ID Q9AVZ
AC Q9AVZ
DT 01-JU
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Best Local
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Best Local &
                                                     Q9AVZ7
Q9AVZ7;
01-JUN-2001
01-JUN-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8IET9;
Q8IET9;
01-MAR-2003
01-MAR-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AL844509; CAD53159.1; -.
Hypothetical protein.
SEQUENCE 2743 AA; 325169 MW; 6FAC4BCD4EF99500 CRC64;
                          Sen1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MAL13P1.13. Name=MAL13P1.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GeneDB_SPombe; SPBC29A10.10c; -.
InterPro; IPR000873; AMP-bind.
PROSITE; PS00455; AMP_BINDING; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate 3D7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T40065; T40065
                                                                                                                                                                                                                                                                                                                  2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1729
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                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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15; Conserv
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|||| | ||:||||||| 1746
IGFLQDLRRLNVALTRAK 1746
                                                                                                                                                                                                                                                                                                            IGFLKDERRLNVALTRAK 2554
                                                                                                                                                                                                                                                                                                                                          1944 AA;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                               (TrEMBLrel.
                                                                                                                                                                       PRELIMINARY;
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A; 222209 MW; 12B005A934BEE11C CRC64;
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                                               Created)
Last sequence update)
Last annotation update)
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Pred. No. 0.00013;
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Pred. No. 0.00019;
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                                                                                                                                                                     692 AA
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Best Local
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EMBL; AJ010592; CAC27074.1; --
PIR; E90113; E90113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guillardia theta (Cryptomonas phi).
Bukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=20087226; Funded-Local J., Penny S.L., Beacon F., Zauner S., Fraunholz M., Wastl J., Penny S.L., Beacon F., Zauner S., Cavalier-Smith T., Maier U., Douglas S.; Cavalier-Smith T., Maier U., Douglas S.; "Chloroplast protein and centrosomal genes, a tRNA intron, and odd "Chloroplast protein and centrosomal genes, the cryptomonal F. The Compact Edwaryotic Genome, the Cryptomonal Chloroplast Protein and Chloroplast
                                                                                                                                                                                                                                                                                                           SEQUENCE
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598
                                                                                                                                               1 Similarity
                                                           IGFLXDXRRINVALTRAK 18
IGFLADGRRINVAFTRAK 615
                                                                                                                                                                                                                                                                                                       692 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                           81812 MW;
                                                                                                                                                                                   91.1%;
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                                                                                                                                                                                           Score 72; 1
Pred. No. 7
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                                                                                                                                                   Mismatches
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